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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1 atgacgactgaaccgttatt.....aatgtatcgtctcccatctg 945
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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c 11	0 80 ~	o o ∗	2 2 2	Result No.
304 304	311.8	311.8	945 320.4	Score 945
32.2	33.0	33.8	100.0 33.9 33.9	Query Match
2 305153	3962 4162 212610	945	216750 36308	Query Match Length DB
21	NNN	9991	222	9 Ed -
AB011838 AP001520	BACORFX BACORFX BSUB0019	AX006205 AX006203	BSUB0007 D88802 BSUB0004	ID 
AB011838 Bacillus AP001520 Bacillus	D45048 Bacillus su 299122 Bacillus su	AX006205 Sequence AX006203 Sequence	299110 Bacillus su D88802 Bacillus su 799107 Bacillus su	Description AX006200 Sequence

PARECIN  288 a 180 c 232 g 245 t  PARIGIN  288 a 180 c 232 g 245 t  PARIGIN  288 a 180 c 232 g 245 t  289 c 245 t  280 c 232 g 245 t  280 c 245 t  280 c 245 g 2	RESULT 1 AX006200 AX006200 AX006200 AX006200 ACCESSION AX006200 AX006200 AX006200 AX006200 SOURCE SOURCE Bacillus subtilis ORGANISM Baccillus subtilis Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus. AUTHE JOURNAL FEATURES FEATURES SOURCE BACTERINCE SOURCE JOURNAL GENENCOR INTERNATIONAL B V (NL); ESTELL DAVID A (US) COTGANISM SOURCE JOURNAL GENENCOR INTERNATIONAL B V (NL); ESTELL DAVID A (US) COTGANISM SOURCE JOURNAL GENENCOR INTERNATIONAL B V (NL); ESTELL DAVID A (US) JOURNAL GENENCOR INTERNATIONAL B V (NL); ESTELL DAVID A (US) JOURNAL GENENCOR INTERNATIONAL B V (NL); ESTELL DAVID A (US) JOURNAL GENENCOR INTERNATIONAL B V (NL); ESTELL DAVID A (US) AUTHORS JOURNAL GENENCOR INTERNATIONAL B V (NL); ESTELL DAVID A (US) TOTAL SOURCE JOURNAL J	12 277.2 29.3 10607 1 AEGOGS10 13 265.8 28.1 1379 3 STREMI 14 252.7 24.0 49997 71 ACCO27136 226 23.9 147006 84 SPNEU1904 227 24.0 23.9 2111 9 ACCO27136 228 23.9 147006 84 SPNEU1904 229 192.4 20.4 49489 76 ACCO259 23 141 14.9 24.3 2 AF259301 24 138.4 14.6 3754 1 AGOCS431 25 189.2 62 3 3883 1 ACCO2631 26 58.2 62 3 3883 1 ACCO2631 27 192.4 20.4 55390 1 ACCO2631 28 59.2 63 3883 1 ACCO2631 29 53.8 60 213732 1 AF201862 29 53.8 5.7 6591 1 AF001952 29 53.8 5.7 6591 1 AF001952 29 53.8 5.7 6591 1 AF001952 29 53.8 5.7 6951 1 AF001952 20 33 38.2 4.0 161528 74 ACC69436 31 43.4 4.6 193378 60 ACC04157 31 38.2 4.0 172064 90 ACC04157 31 38.2 4.0 172064 90 ACC045991 38 38.2 4.0 193378 64 ACC059436 39 38.2 4.0 193378 65 ACC015991 39 38.2 4.0 193378 65 ACC015991 39 38.2 4.0 193378 65 ACC015991 39 38 4.0 188728 92 HASP490024 41 38 4.0 189256 81 ALS9490024 42 37.4 4.0 85356 13 ATF1429 24 37.4 4.0 85356 13 ATF1429 25 37.4 4.0 99814 13 ATF18J2  ALLIGNMENTS  ALLIGNMENTS
RESULT 2 BSCBOO7 LOCUS DEFINITION ACCESSION O; Gaps O; VERSION VERSION VERSION SUBJECT 60 CGGACC 60 CGGANISM SUBJECT 120 REFERENCE AUTHORS	-AUG-2000 Qy 661	AE006310 Lactococc D16594 S.mutans pm AC027136 Staphyloc AF269779 Staphyloc AC07836 Staphyloc AC07830 Staphyloc AC07830 Staphyloc AC07830 Staphyloc AC07830 Staphyloc AF270310 Staphyloc
BSUB0007 216750 bp DNA Bacillus subtilis complete genome (section 7 of 21): from 1194391 to 1411140. Z99110 AL009126 Z99110.1 GI:2633472 Bacillus subtilis. Bacillus subtilis Bacillus subtilis Bacillus subtilis Bacillus subtilis Bacillus subtilis Bacillus Staphylococcus group; Bacillus. 1 (bases 1 to 216750) Kunst,F., Ogasawara,N., Moszer,I., Albertini,A.M., Alloni,G.,	tctattccagaacggcatacagttcaccatgaacaaattgaggatttgcttacaacgaca 720	GCTTTAGCTGATTTTGGCTATACCATTCCGTCACAACGAACAGGGAGTGCTGGGCTTTT 120 gccgcgcatcaaaatggtcaaagcgttgttcaacggaatgtataaggggttcaacgtt [

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Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.

Direct Submission

Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur, Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 7577 Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45 68 89 48
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The complete genome sequence of the gram-positive bacterium Bacillus subtilis

Pacillus subtilis
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ilwishpatimtdeafadeiyfeeltaesltalikkeegdyry
ilwishpatimtdeafadeiyfeeltaesltalikkeegdellaanloggytalnilavel
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Mismatches 0
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Bacillus
D88802
                            Nucleotide sequence and analysis of the phoB-rrnE-groESL the Bacillus subtilis chromosome Microbiology 143 (Pt 6), 1861-1866 (1997) 97346038
                                                                                                                                                                                                                      Direct Submission
Submitted (05-NOV-1996) to the DDBJ/EMBL/GenBank databases. Yoshito Sadaie, National Institute of Genetics, Radioisotope Center; Yata 1111, Mishima, Shizuoka 411, Japan (E-mail:ysadaie@lab.nig.ac.jp, 7el:81-0559-81-6870, Fax:81-0559-81-6870)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               trnA-Asp; trnA-Met; trnA-Gly; trnA-Arg; 5S ribosomal RNA; 16S ribosomal RNA; 23S ribosomal RNA; 241D; groEI; groES; ydLI; yd1 ydLI; 
                                                                                                                                                      2 (sites)
Sadaie,Y., Yata,K., Fujita,M., Sagai,H., Itaya,M.,
                                                                                                                                         Ogasawara,N.
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phoB-rrnE-groESL region,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="ydhB"
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(209) DNA binding"
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lividans
glycosyl transferase; JS0636 (311)"
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Matches
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INLHEAQTFILDHLIYNNGYEBYLAFA
LKAALRHDVISAEDLLKTDQEVLNILRASKNEEVLSLITSIHPGIQVIEDDIQYDFHQ
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tundnvnaiafyqkrgyqfaavffnavekarrlkpeifevaengilirdeilfskvid
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/transl_table=11
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Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A. Direct Submission
Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pastel Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pastel Regulation de l'Expression Genetique, 28 rue du Docteur Roux, Paris Cedex 15, FRANCE B. Email: moszer@pasteur.fr
paris Cedex 15, FRANCE B. Email: moszer@pasteur.fr
paris Cedex 15, FRANCE B. Email: moszer@pasteur.fr
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The complete genome sequence of the gram-positive bacterium Bacillus subtilis
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Yoshida, K., Yoshikawa, H.F., Zumstein, E.,
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complement(1199..1441)
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Alaaclayntsikphnmaisesievltiellselsiknkklkkefagdetvllongki
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bacillus subtilis"
/strain="168"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="ydfT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cransı
                                                                                                                                                              'gene="ydgC'
                                                                                                                                                                                                                                                                                                                                                                  'codon_start=1
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                                                                                                                      proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B. subtilis"
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VICKI GYMTENHKOWSTRYKITSHNIGIEKQLNDYPSERNEREELRLKLETERQE
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3117. .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(5428. .7089)
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complement(5678. .5703)
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/gene="expz"
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/gene="exp2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="ydgf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLGKLSFMTPNDKGYKELDQAFNELTKRIKELDHQDKKD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAB12379.1"
/db_xref="GI:2632873"
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/gene="ydgD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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note="similar to hypothetical proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein_id="CAB12378.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ′gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="similar to amino acid ABC transporter (permease)"
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В δÃ

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118

В Ş

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358

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61

B Ş

562;

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33.9%;

В

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31241 TTCAAACAACGAATAGAAAGCGGTGATTGGAACGGGCTGCTGAGGCGAATCAAAATCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggagaatttaaactcgaaggatatgcagaatgtatcgtctcccatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGGAGATTTCTTTTATGTGCCAAGCGGTACACTCCATGCTTATGTAAGGGAACCCTT
                                                     GGAGAATTTACAATAGAAGGAACATGTGAATTCATGATATCTCATC
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                                                                                                                                                                                                                                                              GTTTATGTGCAATCAGATTATTTCTCAGTGTACAAATGGAAGATTAGCGGCCGAGCTGCT
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                                                                                                                                                                                                                                                                                                                                                      AATGACCAGGGCCAAAAAAGAACTCTTCATATAGAAAAAGCCATGGAAGTCATAACGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ctaactaccatgatagagcgtggagaatgggatgagctcttgcgccgtgtaaaggtaaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9Atgaatatgccaacatacatgaaaacggtgagcttggaaaaacagaatgctggtacatt 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctcagcgaattatgggaacatcacagacatttattcggacagcttgaaggggaccgtttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTTCTGCACATGCCCATGGCTCGTCGTCTGTAAAAAAATGGCCCGCTGGCAGGAAAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tttgccgcgcatcaaaatggtcaaagcgttgttcaaaacggaatgtataaggggttcacg 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTCCTTCATATCAAACCTATTTGCTGGGGAGTGTTCTGAGCGGATCAGGACGAATCATA
                                                                                                                                                                                                                  ttaaagcagcaaaaaccattccttcttatcagtgtgattgaaggggagggccgtatgatc
                                                                                                                                                                                                                                                                                                                                 CCGCATATCGATAAAGTGCATACACCGGAAGTAAAAGAAGTTGGTAACGCTGAGATCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCCTTGAAATCCAGCAAAACTCTGATACAACATATCGCGTATACGATTATGACCGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gctttggagacgcagcagcactcagacccaacctacagattatatgattatgaccgaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTGATTGCAAAGATGACGCCGAACTAATTTTGGGACATCATGCAAGCACAAAGGAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATGATTATGCAAAACTGCACGAAAATGGCGACCTTGGTAAAACGGAGTGCTGGTATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGCTGCTGAAAGCTGCTGGACGCCAATATGGATCTCTCCGTGCAAGTCCATCCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cctctgcttacaaaatattagatgctgaccaggacttatctgttcaggtgcatccgaat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTGATCAAGTATGGAAAGATCATCCAGAGATATTCGGGTTTCCGGATGGTAAGGTGTTT 31060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGCTTCGTGACGCTTTTGGCTACGCAATACCCCTCACAAAAAACAGGTGAGTGCTGGGCC 30940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFVGIELVGLTAGETENPEKVIPKAINNIPVRVLLFYIGALLVIMSIYPWDIINPSES
PFVQVFVAVGIVGAASIINFVVLTSAASACNSAVFSTSRMVYSLAKDHNAPESMAKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 320.4; DB 2; Pred. No. 1.2e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 381;
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                                                 GATTACTATGCCGGAGAAAACGAAGAGGGAGAACTCGGCAAGACGGAATGCTGGTACATT
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Bacillus/Staphylococcus group; Bacillus.
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1 (bases 1 to 3962)

Margot, P., Mauel, C. and Karamata, D.

The gene of the N-acetylglucosaminidase, a Bacillus subtilis 168 cell wall hydrolase not involved in vegetative cell autolysis mol. Microbiol. 12 (4), 535-545 (1994)
                                                                                                                                                                              Direct Submission
Submitted (18-OCT-1993) Vladimir V. Lazarevic, Institut de
Genetique et de Biologie Microbiennes, Rue Cesar-Roux 19,
                                                                                                                                                                                                                                   Vladimir V.
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Bacillus subtilis
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subtilis
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                                              GCTTTACGAGATAGATTTGGATACAGTATTCCTTCAGAATCAACGGGGGAATGCTGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttaaagcagcaaaaaccattccttcttatcagtgtgattgaaggggagggccgtatgatc
                                                                                                                      D45048
D45048.1 GI:1129072
D45048.1 GI:1129072
endo-beta-1,4-glucosaminidase; beta-N-acetylglucosaminidase.
Bacillus subtilis (strain AC327) DNA, clones pEH4 and pWCEV4
Bacillus subtilis
Baciteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                     Bacillus subtilis gene cds.
Bacillus/Staphylococcus group; Bacillus.

1 (bases 1 to 4162)
Margot,P., Mauel,C. and Karamata,D.
The gene of the N-acetylglucosaminidase, a Bacillus cell wall hydrolase not involved in vegetative cell mol. Microbiol. 12 (4), 535-545 (1994)
                                                                                                                                                                                                                                                                             DNA BCT 01-FEB-2000 for beta-N-acetylglucosaminidase, comp
                       subtilis 168
autolysis
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2 (site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sekiguchí, J
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1285. .12
                                                                                                                                                                                                                                                                                                                                                                           /note-"
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                                                                                                                                                                                                                       /gene="
1296. .
                                                                                                                                                                                                                                                                                                                                               /note=
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34..39
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237

456

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417

576 357

636

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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus

(CE 1 (bases 1 to 212610)
RS Kunst, F., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Brousliet, J., Brans, A., Braun, M., Brighell, S.C., Codani, J.J., Connecton, I.F., Cummings, N.J., Carter, N.M., Choi, S.K., Codani, J.J., Connecton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emmerson, P.T., Entlan, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galleron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Gandi, G., Guiseppi, G., Guy, B.J., Haga, K., Haiech, J., Harwood, C.R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F., Klaerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Koningstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Liu, H., Masuda, S., Mauel, C., Medigue, C., Medina, M., Levine, A., Liu, H., Masuda, S., Mauel, C., Medigue, C., Medina, M., Noone, D., O'Reilly, M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Porteelele, D., Porwollik, S., Prescott, A.M., Presecan, E., Pujic, P., Scanlan, E., Rocha, E., Roche, B., Rose, M., Sadaie, Y., Setayuchi, J., Sckowska, A., Seror, S. J., Serror, P., Shin, B.S., Soldo, B., Sorokin, A., Tamakoshi, A., Tanaka, T., Terpstra, P., Tognoni, A., Yasamoto, H., Wedler, E., Westernegger, T., A., Wambutt, R., Wedler, E., Wahler, F., Zusnoto, K., Yata, K., Yata, K., Yata, K., Yata, K., Wata, H., F., Zumanoto, H., Yamane, K., Yata, K., Yat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCGATTTTACGATAAAAGGAACTTGTACCCTTATCGTGTCTCATAT 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATGAGGACAAAACATGTCCGCTCAAAAAAGGTGATCACTTTATTTTGCCGGCCTCAAATG 1116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccgtctattccagaacggcatacagttcaccatgaacaaattgaggatttgcttacaacg 717
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Bacillus subtilis complete
to 3809700
Z99122 AL009126
                                                                                                                                                                                                        The complete genome sequence of the Bacillus subtilis
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                                           Yoshikawa, H. and Danchin, A.
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Regulation de l'Expression Genetique, 28 rue du Docteu
Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr,
adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax:
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1. .212610
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28 rue du Docteur
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Roux, 75724
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                                                      (9093.
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gctttagctgat---tttggctataccattccgtcacaacgaacaggggagtgctgggct 117
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                                                                                                                                                                   ACATTTGTCCAAGGGGAATATTTTTCGGTTTATAAATGGGACATCAATGGCGAAGCTGAA 89738
                                                                        TATGAGGACAAAACATGTCCGCTCAAAAAAGGTGATCACTTTATTTTGCCGGCTCAAATG
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JOURNAL MEDLINE REFERENCE

99184646

Extremophiles 3 (1), 29-34 (1999)

AUTHORS

JOURNAL

REFERENCE

TITLE AUTHORS

COMMENT

Sequence

updated (28-Apr-1998). Location/Qualifiers

.15012

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FEATURES

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KEYWORDS

SOURCE

ORGANISM

Bacillus halodurans clone: ALBAC004. ACCESSION

AB011838 15012 bp DNA Bacillus halodurans C-125 go AB011838

genomic DNA,

AB011838.1 GI:4512380

AB011838

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                                                                                                                                                     AGGAGTTTGGCTACAATATTCCATCCGATAAAACGGGAGAGTGCTGGGCCATTTCTGCTC
                                                                                 Conservative
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VPHQDPDVCPKVTIKDQAVVTTFVETEFFSVHKWDIHGQASFSSDDRYLLVSIIEGTG
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7672. .8619
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/codon_start=1
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/gene="ydhs"
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No. 3.2e-73;
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Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                     Nakasone, K., Hirama, C.,
21-28 (1999)
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TITLE JOURNAL FEATURES SOUICE	JOURNAL MEDLINE REFERENCE AUTHORS	JOURNAL MEDLINE REFERENCE AUTHORS	JOURNAL REFERENCE RETERENCE	JOURNAL REFERENCE AUTHORS	JOURNAL REFERENCE AUTHORS TITLE	AUTHORS TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE	TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL MEDLINE	MEDLINE REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE AUTHORS
Direct Submission Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and Technology Center, Deep-sea Microorganisms Research Group; 2-15 (E-mail:takamih@jamstec.go.jp.) URL:http://www.jamstec.go.jp/jamstec-e/bio/DEEPSTAR/FResearch.html, Tel:81-468-67-3895, Fax:81-468-66-6364) Location/Qualifiers 1.305153 /organism="Bacillus halodurans" /db_xref="taxon:86665"	Characterization and comparative study of the rrn operons of alkaliphilic Bacillus halodurans C-125 Extremophiles 4 (4), 209-214 (2000) 20426005 11 (bases 1 to 305153) Takami, H. and Takaki, Y.	(1,R., Maeno,G., Sa)	kaliphilic bacterium Bacillus mparison with Bacillus subtil 2000)	Biosci. Biotechnol. Biochem. 63, 943-945 (1999)  8 (sites)  Rakami,H., Nakasone,K., Takaki,Y., Maeno,G., Sasaki,R., Masui,N.,  Fuji,F., Hirama,C., Nakamura,Y., Ogasawara,N., Kuhara,S. and  Horikoshi,K.	<pre>(in) Extremophiles in deep-sea environments (Ed.);   HORIKOSHI, K. TSUJII;   249-284; Springer-Verlag (1999) 7 (sites) 7 (sites) 7 Takami, H. and Horikoshi, K. Reidentification of facultatively alkaliphilic Bacillus sp. C-125</pre>	Takami, H., Takaki, Y., Nakasone, K., Sakiyama, T., Maeno, G., Sasaki, R., Hirama, C., Fuji, F. and Masui, N.  Genetic analysis of the Chromosome of alkaliphilic Bacillus halodurans C-125  Extremophiles 3 (3), 227-233 (1999) 99411980 6 (sites) 7akami, H. Genome analysis of facultatively alkalihilic Bacillus halodurans C-125	Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic Bacillus sp. strain C-125 Blosci. Biotechnol. Blochem. 63 (2), 452-455 (1999) 9209008 (sites)  4 (sites)  7akami.H., Masui.N., Nakasone,K. and Horikoshi.K. Replication origin region of the chromosome of alkaliphilic Bacillus halodurans C-125 Blosci. Biotechnol. Biochem. 63 (6), 1134-1137 (1999) 9356711	99184645 2 (sites) Rakami, H., Nakasone, K., Ogasawara, N., Hirama, C., Nakamura, Y., Masui, N., Fuji, F., Takaki, Y., Inoue, A. and Horikoshi, K. Sequencing of three lambda clones from the genome of alkaliphilic Bacillus sp. strain C-125 Extremophiles 3 (1), 29-34 (1999) 99184646 3 (sites) 3 (sites) Takami, H., Takaki, Y., Nakasone, K., Hirama, C., Inoue, A. and Horikoshi, K.
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/note="EVIDENCE BY HOMOLOGY BIO11.02 RNA SYnthesis,
modification, and DNA transcription. COULD PARTICIPATES IN
BOTH THE TERMINATION AND ANTITERMINATION OF TRANSCRIPTION"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="EVIDENCE BY HOMOLOGY BIO15.02 HYPOTHETICAL. Conserved. 50% identical to PH1801 of Pyrococcus horikoshii."
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/gene-"yhhD"
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TSVLGGPLLKLERITDPVAQGIALGGTGHAVGTGTAIELGKTQGAMAALSIGVTGIMY
VIFAPIIAKIILGY"
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                                                                                                                                                      note-"EVIDENCE BY
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"L173813"
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7173...7532
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LAPDYD"
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                                                           GGCGACAAAGTCCCTGAAAATCAATTTAAAAACTGAAAAATTTGCTGATGCAAAAAATTACA
                                                                                                                                                                                                                                                                                                  ttggagacgcagcagaactcagacacaacctacagattatatgattatgaccgaaaaagat
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/protein_id="AAK04868.1"
/protein_id="AAK04868.1"
/db_xxref="G1:12723688"
/translation="MKTDDFDKVEWLIQLEHDEMILEEQFLKDSAYSDVTVKELQILT
LYHTLGTCRATDIAKNOKLAGFITTTLURLEDKGYIERKRSTADRRVTHIILTSKGD
ELDATHREFFHTITDNLFDSYYGTTENKLAGELATLHDSLENMK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Biochemistry
Tokyo Dental College
1-2-2 Masago, Mihama-ku
Chib. Chib.
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1;121(1):130]]
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                                                                                                                                                                                                                                                                                                                 Submitted (05-JUL-1993) to the DDBJ/EMBL/GenBank databases. Yutaka Sato, Tokyo Dental College, Dept. of Biochemistry; 2-2 Masago 1-chome, Mihama ku, Chiba, Chiba 261, Japan (Tel:043-279-2222, Fax:043-279-2052)
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gattttttctatgtgccaagcggtactgttcatgcgattggaaaaggaattcttgctttg
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                                                                                                                                                                                                                                                                                                                                 accatgatagagcgtggagaatggggatgagctcttgcgccgtgtaaaggtaaagccgggg
                                           GATTTCTTCTATGTTCCTAGTGGCACTATGCATGCCATTGGTAGGGGAATTATGATTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGATGAAGGTGCTGAAATTATCTATGGACACGAAGCTAAATCTAAAGAAGAATTGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ag--ctgattttggctataccattccgtcacaacgaacaggggagtgctgggcttttgcc 123
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1309. .1314
1332. .1337
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/protein_id-"BAA04021.1"
/protein_id-"BAA04021.1"
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ALEHGGELGKTECWYVISADEGAEITYHFAKKSEFLOWIAAGDWDHLITKIPVAG
DFFYVPSGTMHAIGRGHILETGYGSSDYTYRWQISGSYKMQQTAPYLLVSVLAGQGRI
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230. .234
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/db_xref="GI:451215"
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/transl_table=11
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                                                                                                                                                                                                                         ok 73019, USA
on Jun 15, 2000 this sequence version replaced g1:8225121.
on Jun 15, 2000 this sequence version replaced g1:8225121.
on Jun 15, 2000 this sequence version replaced g1:8225121.
on Jun 2015 this sequence if currently
consists of l contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
1, 49897 toottly of 49897 bp in length.
10catton/qualifiers
1. 49897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Loh, P., Q1.S., Ray, L., Ford, B., Iondola, J. and Roe, B.A.
Direct Submission
Submitted (28 MAR-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus/Staphylococcus group; Staphylococcus.

1 (Dases 1 to 4987)

Loh.P., Ol.S., Ray.L., Ford.B., Worrell,V., Iandolo,J. and Roe,B.A.

Staphylococcus aureus BAC Clone sabac-106

Unpublished
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HTGS_PHASE2; HTGS_DRAFT
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/db_ref="taxon:106"
/clone="sabac-106"
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/clone_11b="OU staph library"
/ 9237 c 7267 g 17640 t
                    26.7%;
Score 252.2; DB 71; Length Pred. No. 7.6e-59; 0; Mismatches 418; Indels
                2; DB 71;
7.6e-59;
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.

1 (bases 1 to 2815)
Kimmerly,W.J., Taylor,J.David, Nelsen,A.J., Godlevski,M.M.,
Rubino,M.A., Nelson,F.J., Rivers,P.R., Torruella-Miller,I.,
Listenbee,S., Ashanti,C., Altshuller,G., Mamo,L., Shepherd,J.
Fuchs,R., Fleming,T., Guan,X., Du,L., Cain,D.H., Miller,G.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (22-MAY-2000) Departments of Genomic Sciences and Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc., 5 Drive, Research Triangle Park, North Carolina 27709-3398, USA 1. .2815
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3.3e-135
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gb_ba3:STPMIPHI
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gb_pat1:AX065227
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AUTHORS
TITLE
JOURNAL
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KEYWORDS
SOURCE
ORGANISM
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Quality: 1692.00
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LOCUS AX0062
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Macillus subtilis

Bacillus subtilis

1 (Dases I to 945)

Estell D.A.

1 (Dases I to 945)

Estell D.A.

1 (Dases I to 945)

Estell D.A.

Proteases from gram-positive organisms

Proteases from gram-positive organisms
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I X57117 S.typhimurium pmi ge
I AE004115 Vibrio cholerae c
I Z48229 S.cerevisiae tRNA-Va
I AX065227 Sequence 353 from
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LOCUS BSUB0007 2
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Bacillus subtilis.

ISM Bacillus subtilis.

Bacteria; Firmicutes; Bacillus/Clostridium group;

Bacteria; Firmicutes; Bacillus/Clostridium group;

Bacteria; Firmicutes; Bacillus/Clostrini,A.M., Alloni,G.,

Bacteria; Firmicutes; Bacillus.

CE 1 (bases 1 to 216750)

CE 1 (bases 1 to 216750)

Azevedo,V., Bertero,M.G., Bessieres,P., Bolotin,A., Borchert,S.,

Borniss,R., Boursier,L., Brans,A., Braunn,M., Berghell,S.C.,

Borniss,R., Boursier,L., Brans,A., Braunn,M., Brignell,S.C.,

Carter,N.M., Choi,S.K., Codani,J.J., Connerton,I.F., Cummings,N.J.,

Daniel,R.A., Denizot,F., Devine,K.M., Dusterhoft,A., Ehrlich,S.D.,

Emmerson,P.T., Entian,K.D., Errington,J., Fabret,C., Ferrari,E.,

Foulger,D., Fritz,C., Fujita,M., Fujita,Y., Fuma,S., Galizzi,A.,

Galleron,N., Ghim,S.Y., Glaser,P., Goffeau,A., Golightly,E.J.,

Galleron,N., Ghim,S.Y., Glaser,P., Goffeau,A., Golightly,E.J.,

Galleron,N., Jones,L., Holsappel,S., Hosono,S., Hullo,M.F.,

Itaya,M., Jones,L., Joris,B., Karamata,D., Kasahara,Y.,

Koningstein,G., Krogh,S., Kumano,M., Kurita,K., Lepidus,A.,

Lardinols,S., Lauber,J., Lazarevic,V., Lee,S.M., Levine,A., Liu,H.,
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genome (section 7 of 21): from 1194391
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MEDLINE
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TITLE
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Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.

Direct Submission

Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur, Regulation de 1'Expression Genetique, 28 rue du Docteur Roux, 7572

Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
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                Mauel, C., Medigue, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medina, N., Mellado, R.P.
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(subunit B)"
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gene

gene

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Percent Similarity:

alignment\_block: US-09-462-846-2 x BSUB0007 Percent

Align seg 1/1 to: BSUB0007 from: 1 to: 216750

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80023

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CDS gene

pTyrIleIleAspCysGlnLysAspAlaGluIleIleTyrGlyHisAsnA 134 80173

134 laThrThrLysGluGluLeuThrThrMetIleGluArgGlyGluTrpAsp 150

JOURNAL JOURNAL OMMENT EATURES SOURCE				seg_documentation LOCUS AB011 DEFINITION Bacil ACCESSION AB011 VERSION AB011	seq_name: g	301 G1 11 80674 GA	284 al 11 80624 TC	267 uL    80574 TC	251 Ly      80524 AA	234 lu      80474 AG	217 eG    80424 AG	201 A1      80374 GC	184 ln      80324 AG	167 os      80274 AA	151 G1      80224 GA	80174 CA
Direct Submission Direct Submission Submitted (04-MAR-1998) to the DDBJ/EMBL/GenBank databases. Hideto Takami, Japan Marine Science and Technology Center, Deep-sea Microorganisms Research Group; 2-15 Natsushima, Yokosuka, Kanagawa 237, Japan (E-mail:takamih@jamstec.go.jp, Tel:81-468-67-3895, Fax:81-468-66-6364) Sequence updated (28-Apr-1998). Location/Qualifiers 115012	Extremophies 3 (1), 29-34 (1999) 99184646 2 (bases 1 to 15012) Takami,H. and Inoue,A.	l (sites) Takami,H., Nakasone,K., Ogasawara,N., Hirama,C., Nakamura,Y., Masui,N., Fuji,F., Takaki,Y., Inoue,A. and Horikoshi,K. Sequencing of three lambda clones from the genome of alkaliphilic Bacillus sp. strain C-125	Bacillus halodurans (strain:C-125) DNA, clone_lib:lambda no.4 clone:ALBAC004. Bacillus halodurans Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillaceae; Bacillus.	tation_block: AB011B38 15012 bp DNA AB011B38 15012 bp DNA Bacillus halodurans C-125 genomic DNA, 6A fragment, clone ALBAC004. AB011B38 AB011B38 GI:4512380	gb_ba1:AB011838	GluPheLysLeuGluGlyTyrAlaGluCysIleValSerHisLeu 315 	alTyrProPheLysLysGlyAspHisMetLeuLeuProTyrGlyLeuGly 300 	uLeuIleSerValIleGluGlyGluGlyArgMetIleSerGlyGluTyrV 284 	LysTrpAsnLeuSerGlySerAlaSerLeuLysGlnGlnLysProPheLe 267 	luAspLeuLeuThrThrLeuIleGluCysAlaTyrPheSerValGly 250 	eGluValProSerIleProGluArgHisThrValHisHisGluGlnIleG 234 	AlaGluGlyLysLeuArgGluLeuHisLeuLysLysSerIleGluValII 217 	InGlnasnSeraspThrThrTyrArgLeuTyrAspTyrAspArgLysasp 200 	OSETGlyThrValHisAlaIleGlyLysGlyIleLeuAlaLeuGluThrG 184 	GluLeuLeuArgArgValLysValLysProGlyAspPhePheTyrValPr 167 	CAACAACAAAGGAAGAACTAACTACCATGATAGAGCGTGGAGAATGGGGAT 80223
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CDS RBS

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8
                                                                                                                                                                                                                                                                                            B.subtilis ydhS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B.subtilis ydhQ gene(53%-identity)"
                                                                                                                                                                                                                                                                                            gene(53-69% identity)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
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                                                                                                                                                                            119
                                                                                                                                                                                                                                                                                                103
                                                                                                                                                                                                                                                                                                                                                                                                                86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 luCysTrpAlaPheAlaAlaHisGlnAsnGlyGlnSerValValGlnAsn
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Ratio:
t Similarity:
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|:::||||||:::||
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complement(10733...10737)
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Percent Identity: 57.595
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7727

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136 8027

8077

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7927 86 7877 69 7827 52 7777

JOURNAL Extremophiles 3 (1), 21-28 (1999)  MEDLINE 99184645  REFERENCE 2 (sites) AUTHORS Takami.H., Nakasone,K., Ogasawara,N., Hirama,C., Nakamura,Y.,  Masui.N., Fuji.F., Takaki,Y., Inoue,A. and Horikoshi,K.  Sequencing of three lambda clones from the genome of alkaliphilic sacillus sp. strain C-125 Bacillus sp. strain C-125  MEDLINE Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic Bacillus sp. strain C-125  JOURNAL Biosci. Biotechnol. Biochem. 63 (2), 452-455 (1999)	AP001520 305153 bp DNA Bacillus halodurans genomic Ap001520 BA000004 AP001520.1 GI:10176401 Bacillus halodurans DNA. Bacillus halodurans Bacillus halodurans Bacteria; Firmicutes; Bacil Bacillus/Staphylococcus gro 1 (sites) 1 (sites) Takami, H., Nakasone, K., Hir Nakamura, V. and Inoue, A. An improved physical and ge Bacillus gp. C-125	299 LeuGlyGluPheLysLeuGluGlyTyrAlaGluCysIleValSerHis 314 :::::::::   ::::    ::::	265 oPheLeuLeuIleSerValIleGluGlyGluGlyArgMetIleSerGlyG 282 :::     :::  :::	IntegluaspleuLeuThrThrThrThrLeuTlegluCysAlaTyrPhesor ::::::::::::::::::::::::::::::::::::	153 LeuArgArgValLysProGlyAspPhePheTyrValProSerg1 169 [      :::
gene CDS	MOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL SOURCES SOURCE	JOURNAL MEDLINE REFERENCE AUTHORS TITLE	TITLE JOURNAL REFERENCE AUTHORS TITLE	REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS	REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE REFERENCE RUTHORS TITLE JOURNAL MEDLINE RUTHORS JOURNAL
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US-09-462-846-2 x AP001520/rev
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155351 CAACCGATTTTTTAACACCTGTGTTTAAGGAGCGTATTTGGGGAAGGAC 155302
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Gaps: 3
Percent Identity: 57.595
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36

155252

155202

CDS gene

gene

gene

169

154902

154952

155002

155052

Sgo

CDS gene gene

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REFERENCE
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                             us-09-462-846-2 x Ax006203
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Align seg 1/1 to: AX006203
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 lnIleGluAspLeuLeuThrThrLeuIleGluCysAlaTyrPheSer 248
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Bacillus subtilis
Bacitlus/Clostridium group;
Bacteria; Firmioutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
1 (bases 1 to 948)
                                                                                                                                                                                                                     Proteases from gram-positive organisms
Patent: WO 9904016-A 4 28-JAN-1999;
GENENCOR INTERNATIONAL B V (NL); ESTELL DAVID A (US)
LOCATION/Qualifiers
1. 948
                                                                                                                                                                                                                                                                                                                                                                                                            AXUU6203 948 bp DNA
Sequence 4 from Patent WO9904016.
AXO06203
                                                                                                                                                                                                                                                                                           Estell, D.A.
                                                                                                                                                                                                                                                                                                                                                                                                AX006203.1 GI:9929072
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3.822
81.013
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                                                                      Gaps: 1
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SOURCE
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VERSION
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Bacillus subtilis
Bacteria; Firmicutes; Bacillus/Clostridium group;
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1 (bases 1 to 3962)
Margot,P., Mauel,C. and Karamata,D.
Margot,e., Mauel,C. and Karamata,D.
The gene of the N-acetylglucosaminidase, a Bacillus subtilis 168
cell wall hydrolase not involved in vegetative cell autolysis
cell microbiol. 12 (4), 535-545 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-OCT-1993) Vladimir V. Lazarevic, Institut de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vladimir V. Lazarevic., TITLE Direct Submission
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                                                                             _number="3.2.1.30"
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BASE COUNT
ORIGIN
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us-09-462-846-2 x BSU02562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 CAACGGGGGAATGCTGGGCCATTTCCGCTCATCCAAAAGGACCGAGCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 hrLysIleLeuAspAlaAspGlnAspLeuSerValGlnValHisProAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 ValGlnAsnGlyMetTyrLysGlyPheThrLeuSerGluLeuTrpGluHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 rgThrGlyGluCysTrpAlaPheAlaAlaHisGlnAsnGlyGlnSerVal 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 pGlyGlyThrAlaLeuAlaAsp...PheGlyTyrThrIleProSerGlnA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAAGCTGCTGGATGTGAAGGAAGATACGTCAATTAAAGTTCACCCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sHisArgHisLeuPheGlyGlnLeuGluGlyAspArgPheProLeuLeuT
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AspGluLeuArgArgValLysValLysProGlyAspPhePheTyrVa
                                                                                   CGGCCCGCTCAAAAACCGAACTTGTCACAATGATCAACAGCGGTGACTGG
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                                                                                                                                                                                                    CTGGTACATTATCGACTGTAAGGAAAACGCAGAAATCATTTACGGGCATA 585
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VNRWYSLYSLLDGYTLYFDVPEYR"
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Gaps: 1
Percent Identity: 56.646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leGluAspLeuLeuThrThrThrLeuIleGluCysAlaTyrPheSerVal 249
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D45048

D45048

D45048.1 GI:1129072

Endo-beta-1,4-glucosaminidase; beta-N-acetylglucosaminidase.

Bacillus subtilis

Bacillus subtilis

Bactllus systaphylococcus group; Bacillus.

Bacillus/Staphylococcus group; Bacillus.

1 (bases 1 to 4162)

Margot,P., Mauel,C. and Karamata,D.

Margot,P., Mauel,C. and Karamata,D.

The gene of the N-acetylglucosaminidase, a Bacillus subtilis 168

Tell wall hydrolase not involved in vegetative cell autolysis

Mol. Microbiol. 12 (4), 535-545 (1994)
                                                Rashid,M.H., Mori,M. and Sekiguchi,J.
Glucosaminidase of Bacillus subtilis: cloning, regulation, primary structure and blochemical characterization
Microbiology 141 (Pt 10), 2391-2404 (1995)
96036197
3 (bases 1 to 4162)
96kiguchi,J.
10irect Submission
Submitted (07-JAN-1995) to the DDBJ/EMBL/GenBank databases. Junichi submitted (07-JAN-1995) to the DDBJ/EMBL/GenBank dupiversity, Department of Applied Biology; 3-15-1 Tokida, Ueda-shi, Nagano 386, Japan (E-mali)jeskiguegiptc.shinshu-u.ac.jp, Tel:0268-21-5344, Fax:0268-21-5331)
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Bacillus subtilis gene
   Location/Qualifiers
1. .4162
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1296 .1
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FC_number-"3.2.1.30"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="pEH4 and pWCEV4" 34. .39
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/note="rho-independent terminator"
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         between
         GLCNAC
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alignment_block:
US-09-462-846-2 x BACORFX
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ## 17 GCACCGTGAAGTATTCGGCGGCGTAGAGGGGGATCGGTTTCCGCTTCTGA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367
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216 lileGluValProSerIleProGluArgHisThrValHisHisGluGlnI 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pGlyGlyThrAlaLeuAlaAsp...PheGlyTyrThrIleProSerGlnA 33
                                                                                                         GCCGAGCGGAACGCTGCACGCATTGTGCAAGGGGGCCCTTGTTTTAGAGA
                                                                                                                                                                                                                                                           GAGGGCCTGCTGCGAAGAATCAAAATTAAACCGGGTGATTTCTATTATGT 716
                                                                                                                                                                                                                                                                                                                                                                                                        CTGGTACATTATCGACTGTAAGGAAAACGCAGAAATCATTTACGGGCATA 616
                                                                                                                                                                                                                                                                                                                                                                                                                            STrpTyrIleIleAspCysGlnLysAspAlaGluIleIleTyrGlyHisA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATTACTATGCCGGAGAAAACGAAGAGGGAGAACTCGGCAAGACGGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspGluTyrAlaAsnIleHisGluAsnGlyGluLeuGlyLysThrGluCy 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hrLysIleLeuAspAlaAspGlnAspLeuSerValGlnValHisProAsn 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTGCAAATGGCCCGTATAAAGGAAAGACATTGATCGAGCTTTGGGAAGA 416
                                                              AspAlaGluGlyLysLeuArgGluLeuHisLeuLysLysSerIleGluVa 216
                                                                                                                                                                                                                     lProSerGlyThrValHisAlaIleGlyLysGlyIleLeuAlaLeuGluT 183
                                                                                                                                                                                                                                                                                     AspGluLeuLeuArgArgValLysValLysProGlyAspPhePheTyrVa 166
                                                                                                                                                                                                                                                                                                                                 CGGCCCGCTCAAAAACCGAACTTGTCACAATGATCAACAGCGGTGACTGG
                                     GATAGCAACGGAAGTCCGAGAGAGCTTCATTTTGCCAAAGCGGTCAATGC
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Ratio:
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81.013
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JOURNAL
MEDLINE
REFERENCE
AUTHORS
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VERSION
KEYWORDS
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LOCUS BSUB0019 2
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ORGANISM
                                                                                                                                                               TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               917 GAAAAGGAATAACCATTAAAACATTTGTCCAAGGGGAATATTTTTCGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 GlyLysTrpAsnLeuSerGlySerAlaSerLeuLysGlnGlnLysProPh 266
                                                                                                                                                                                                    Azevedo, V., Bertero, M.G., Bessleres, P., Bolotin, A., Borchert, S., Bruriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Browillet, S., Bruschi, C.V., Caldwell, B., Capuano, V., Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emmerson, P.T., Entian, K.D., Errington, J., Fabet, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galieron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Garandi, G., Guiseppi, G., Guy, B.J., Haga, K., Haiech, J., Harwood, C.R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y., Klaerr, Flanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Koningstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Lardinois, S., Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Mauel, C., Medique, C., Medina, N., Mellado, R., P., Masuda, S., Mauel, C., Medique, C., Medina, N., Mellado, R., P., Masuda, S., Mauel, C., Medique, C., Medina, N., Mellado, R., P., Portetelle, D., Porwollik, S., Prescott, A.M., Noone, D., O'Reilly, M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Persecan, E., Pujic, P., Puro, P., Schlach, S., Schroeter, R., Scoffone, F., Sekiguchi, J., Scanlan, E., Schleich, S., Schroeter, R., Scoffone, F., Sekiguchi, J., Scokin, A., Tanaka, T., Tarbashi, H., Takamaru, K., Vashida, K., Yallamoto, H., Yamanoto, H., Yamanoto, K., Yata, K., Yoshikawa, H. F., Zumstein, E., Yoshikawa, H. and Danchin, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus subtilis.
Bacillus subtilis
Bacillus firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.

1 (bases 1 to 212610)
1 (bases 1 to 212610)
Noszer, I., Albertini, A.M., Alloni, G.,
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Z99122.1 GI:26
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Bacillus subtilis
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                                                                                   Bacillus subtilis
Nature 390 (6657), 249-256 (1997)
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                                                                                                                                                            The complete genome sequence of the gram-positive bacterium
                                                                                                                                                                                            Danchin, A
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19 of 21): from 3597091
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2 (bases 1 to 212610)
Kunst, F., Ogasawara, N.,

Yoshikawa, H.

and Danchin, A.

98044033

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur, Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: moszerépasteur.fr, adanchinépasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45 68 89 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submission
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US-09-462-846-2 x BSUB0019/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                 90117
89867 CGCCACGGTTCCCCATGTGGACGGGTATATAGATGAATCGACAGAATCAA 89818
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                                216 lIleGluValProSerIleProGluArgHisThrValHisHisGluGlnI 233
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cgecccgcTcAaAAAccgAacTTGTCACAATGATCAACAGCGGTGACTGG 900
                                                                                                                                                                                                                                                                                                                                                                                                                                      GCACCGTGAAGTATTCGGCGGCGTAGAGGGGGGATCGGTTTCCGCTTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValGlnAsnGlyMetTyrLysGlyPheThrLeuSerGluLeuTrpGluHi 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rgThrGlyGluCysTrpAlaPheAlaAlaHisGlnAsnGlyGlnSerVal 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pGlyGlyThrAlaLeuAlaAsp...PheGlyTyrThrIleProSerGlnA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MetThrThrGluProLeuPhePheLysProValPheLysGluArgIleTr 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAAGCTGCTGGATGTGAAGGAAGATACGTCAATTAAAGTTCACCCTGAT 90218
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                                                                                                                                                                                                                                                  lProSerGlyThrValHisAlaIleGlyLysGlyIleLeuAlaLeuGluT
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6
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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS AX006205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_pat1:AX006205
                                                                                                                                                                                                                                                                                                              us-09-462-846-2 x AX006205
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AX006205
                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89617 CCCGATTTTACGATAAAAGGAACTTGTACCCTTATCGTGTCTCATATT 89570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89667 AAACATGTCCGCTCAAAAAGGTGATCACTTTATTTTGCCGGCTCAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89767 TATAAATGGGACATCAATGGCGAAGCTGAAATGGCTCAGGATGAATCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 leGluAspLeuLeuThrThrLeuIleGluCysAlaTyrPheSerVal 249
                                                                                        source
                                154
                                                            52
                                                                                                                                                                                       19
                                                                                                                                                        54 GACGAAGCTTCGTGACGCTTTTGGCTACGCAATACCCTCACAAAAAAACAG
                                                                                                                                                                                                                   eLeuLeuIleSerValIleGluGlyGluGlyArgMetIleSerGlyGluT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyGluPheLysLeuGluGlyTyrAlaGluCysIleValSerHisLeu 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTGATTTGCAGCGTGATAGAAGGAAGCGGTTTGCTCAAGTATGAGGACA 89668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyLysTrpAsnLeuSerGlySerAlaSerLeuLysGlnGlnLysProPh
                                                                                                                                                                       YThralaLeuAlaAsp...PheGlyTyrThrIleProSerGlnArgThrG 35
gHisLeuPheGlyGlnLeuGluGlyAspArgPheProLeuLeuThrLysI 85
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                                                         AsnGlyMetTyrLysGlyPheThrLeuSerGluLeuTrpGluHisHisAr 68
                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus subtilis.
Bacillus subtilis
Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
1 (bases 1 to 945)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6 from Patent
Ax006205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteases from gram-positive organisms Patent: WO 9904016-A 6 28-JAN-1999; GENENCOR INTERNATIONAL B V (NL); ESTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Estell, D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AX006205.1 GI:9929073
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189 c 223 g 243 t
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3.804
80.511
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                                                                                                                                                                                                                                                                                                                                                           Gaps:
Percent Identity:
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WO9904016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NL); ESTELL DAVID
                                                                                                                                                                                                                                                                                                                                                             55.591
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                                                                                                                                                         103
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seq_documentation_block:  DA DEFINITION Bacillus subtilis DNA for phoB-rrnE-groESL region, complete cds.  ACCESSION Bacillus subtilis DNA for phoB-rrnE-groESL region, complete cds.  ACCESSION DB8802.1 GI:1945083  VERSION TRNA-ASP, tRNA-MET, tRNA-Gly: tRNA-Arg; 5S ribosomal RNA; 16S ribosomal RNA; 23S ribosomal RNA; 23S ribosomal RNA; 24S ribosomal RNA; 25S ribosomal RNA;	seq_name: gb_ba2:D88802	302 PheLysLeuGluGlyTyrAlaGluCysIleValSerHis 314      :::       :::	285 yrProPheLysLysGlyAspHisMetLeuLeuProTyrGlyLeuGlyGlu 301 	268 uileSerVallleGluGlyGluGlyArgMetIleSerGlyGluTyrValT 285          ::::::   :::   ::::     606GAGTGTTCTGAGCGGATCAGGACGAATCATAAATAATGGTATTCAGT 853	252 TrpAsnLeuSerGlySerAlaSerLeuLysGlnGlnLysProPheLeuLe 268    :::::         ::::: :: :: :: !:      754 TGGAAGATTAGCGGCCGAGCTGCTTTTCCTTCATATCAAACCTATTTGCT 803	235 spleuleuThrThrLeuIleGluCysAlaTyrPheSerValGlyLys 251 ::	218 uValProSerIleProGluArgHisThrValHisHisGluGlnIleGluA 235 :::             ::	202 GluGlyLysLeuArgGluLeuHisLeuLysLysSerIleGluValIleGl 218 :::   :::	185 lnAsnSerAspThrThrTyrArgLeuTyrAspTyrAspArgLysAspAla 201 	168 rGlyThrValHisAlaileGlyLysGlyIleLeuAlaLeuGluThrGlnG 185 	152 LeuLeuArgArgValLysValLysProGlyAspPhePheTyrValProSe 168 	135 hrThrLysGluGluLeuThrThrMetIleGluArgGlyGluTrpAspGlu 151 ::	118 rIleIleAspCysGlnLysAspAlaGluIleIleTyrGlyHlsAsnAlaT 135 	TyrAlaAsnIleHi9GluAsnGlyGluLeuGlyLysThrGluCysTrpTy         :::::         :::	85 leLeuAspAlaAspGlnAspLeuSerValGlnValHisProAspAspGlu 101 ::	:::::        AGAGATATTCGGGTTTCCGGATGGTAAGGTGTTTCCGCTGGTAAAGC
694.1" 66" KLDKPTPYYLOFYNOLKKMIENGTFKPGE KLDKDDRNGFSITSLTAKDVDEIYKIRIP KALHNGTEDTEIIRLNOKFHELLVDFSHN		FTELMPKYULKSSHLEDSGDCRPAVVILNKTKNLTSCQVFL"  gene 18892563 /gene="ydhc" 7989 2663	/UL_ALET GET AF JOEG //ULANS LATION ** MALIILVMELLGIILGE IGAGGAGEVIALLTLLEHIPIHTALGTS //ULANS LATION ** MALIILVMELLGIILGE IGAGGAGEVIALLTSE IPADLLHYLTAG LAGMAFTSLSGAYSHYREGNIQMKIGLIVGGFAAVGAKTAGVISGTEGIGSAPEIQJG MLELSALILLIRUETLEKKAQVVQSTLSTYTRAVILGIAAGVUSGTEGIGSAPEIQJG IMTMI,NISTREGNIGTMYNJY IDPLAVGGGTGYTTEGYTTEGYVDAYLTAVINGAYVGAK	/ NOCE TABLE IN THE CONTROL OF THE C	/gene="ydhb" complement(861. /gene="ydhB"	FGGIIHEKSLLRIAVITAMIATAVLLTWTMIHGPLATLVISIFIYMITIGMVLTSTFT LAMEKQGHRAGSASALLGMLPLLLGSIVSPLVGINETTAVPMGAIMFVTAVIGSLAFF GLTKERVGONS* GCOMD Lement (8611640)	/db_xref="g1:1945084" /db_xref="g1:1945084" /tianslation="AGIVISRAIVROUETGRELSKEPSSLIMVITAVAPMVGGAI /tianslation="AGIVISRAIVROUETGRELSKEPSSLIMVITAVAPMVGGAI LLLPFATWHTIFHVMIIGELLVULIALRLKETLPSSIGTSVKTMSSLIKGR SYMGYALTVGFTHGGSFAYVGGTPFVYODTVGVSDOVPSSILFGTNGLAITGGSFTTGS	(694) transmembrane"  /codon_start=3 /transl_table=1 /rransl_table=1	gK"	/str /sub /db_	FEATURES Location/Qualifiers  136308 Source /organism="Bacillus subtilis" //cgalisc="Idea" subtilis"	TITLE Nucleotide sequence and analysis of the phoB-rrnE-groESL region of the Bacillus subtilis chromosome JOURNAL Microbiology 143 (Pt 6), 1861-1866 (1997)	Tel:81-0559-81-6870, Fax:81-0559-81-6870)  REFERENCE 2 (sites)  AUTHORS Sadaie, Yata, K., Fujita, M., Sagai, H., Itaya, M., Kasahara, Y. and	TITLE Direct Submission  JOURNAL Submitted (05-NOV-1996) to the DDBJ/EMBL/GenBank databases. Yoshito Sadaie, National Institute of Genetics, Radioisotope Center; Yata 1111, Mishima, Shizuoka 411, Japan (B-mail:ysadaieelab.nig.ac.jp,	to 36308) ata,K., Fujita,M., Sagai,H., Itaya,M	DNA.  ORGANISM Bacillus subtilis  Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillaceae;

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gene
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US-09-462-846-2 x D88802
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   83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="B. subtilis yxaR hypothetical protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="secretory"
                                                                                                                                                                                                                                                                                                                                                 .10369
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Align seg 1/1 to: D88802 from: 1
                                                                                                                                                                                                                                                                                             17879 GACGAAGCTTCGTGACGCTTTTGGCTACGCATACCCCTCACAAAAAACAG 17928
                                                                                                                                                                                                                                                                                                                                                                                                 17829 ACGCATCCATTATTTTAGAGCCTGTCTTTAAAGAAAGACTATGGGGAGG
                                                                                                                                                                                                                                35 lyGluCysTrpAlaPheAlaAlaHisGlnAsnGlyGlnSerValValGln 51
                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ThrGluProLeuPhePheLysProValPheLysGluArgIleTrpGlyGl
                           gHisLeuPheGlyGlnLeuGluGlyAspArgPheProLeuThrLysI 85
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                                                                                                                                       AsnGlyMetTyrLysGlyPheThrLeuSerGluLeuTrpGluHisHisAr 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            958.50
3.804
80.511
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Percent Identity: 55.591
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18078
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VERSION
KEYWORDS
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                                                                                                                        SOURCE
                                                                                                                                                                               ACCESSION
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                                                                                                                                                                                                                                                                                        seq_name: gb_ba2:BSUB0004
                           AUTHORS
                                                                                                     ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                    uValProSerIleProGluArgHisThrValHisHisGluGlnIleGluA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTACAATAGAAGGAACATGTGAATTCATGATATCTCAT 18767
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                                                                                                                                                                                                                                                                                                                                                                                                                                        yrProPheLysLysGlyAspHisMetLeuLeuProTyrGlyLeuGlyGlu 301
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Bacillus subtilis.

Bacillus subtilis

Bacillus/Staphylococcus group; Bacillus/

Bacillus/Staphylococcus group; Bacillus.

1 (bases 1 to 21319)

Kunst, F., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert,
                                                                                                                                                                                                          Bacillus subtilis
                                                                                                                                                                             AL009126
                                                                                                                                                            GI:2632866
                                                                                                                                                                                                                bp DNA BCT 26-NOV-1997 complete genome (section 4 of 21): from 600701 to
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      Borchert, S.,
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MEDLINE
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
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Borriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Brons, S., Brouillet, S., Bruschi, C.V., Caldwell, B., Capuano, V., Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emmerson, P.T., Entian, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, V., Fuma, S., Galizzi, A., Galleron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Grandi, G., Guiseppi, G., Guy, B.J., Hagawa, K., Haiech, J., Harwood, C.R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F., Klaerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Koningstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Lardinois, S., Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Mauel, C., Medique, C., Medina, N., Mellado, R.P., Mizuno, M., Moestl, D., Nakai, S., Noback, M., Noone, D., O'Reilly, M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Ogawa, K., Schleich, S., Schroeter, R., Scoffone, F., Sekiguchi, J., Schousha, E., Rocche, B., Rose, M., Sadaie, Y., Sato, T., Sconlan, E., Schleich, S., Schroeter, R., Scoffone, F., Sekiguchi, J., Seroor, P., Shin, B.S., Soldo, B., Sorokin, A., Tanakoshi, A., Tanaka, T., Terpstra, P., Tognoni, A., Viani, A., Wedler, E., Wedler, E., Wedler, E., Vasasrotti, A., Wandutt, R., Wedler, E., Wander, F., Vasasrotti, A., Vannier, E., Wipat, A., Yamamoto, H., Yamane, K., Yasumoto, K., Yata, K., Yata, K., Yoshikawa, H.F., Zumstein, E., Yoshikawa, H. and
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Kunst,F., Ogasawara,N., Yoshikawa,H. and Danchin,A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (18.NOV-1997) I. Moszer, A. Danchin, Institut Pasteur, Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45 68 89 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The complete genome sequence of the gram-positive bacterium Bacillus subtilis
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                        terminator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERIIQLPEAAETHLLQIQLLNGLLHISYPRQVETVAFNKGL"
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leLeuAspAlaAspGlnAspLeuSerValGlnValHisProAsnAspGlu 101
                                                AGAGATATTCGGGTTTCCGGATGGTAAGGTGTTTCCGCTGCTGGTAAAGC
                                                                                                                                        AATGGCCCGCTGGCAGGAAAGACACTTGATCAAGTATGGAAAGATCATCC
                                                                                                                                                                                                                                   GTGAGTGCTGGGCCGTTTCTGCACATGCCCATGGCTCGTCGTCTGTAAAA
                                                                                                                                                                                                                                                                                                                              GACGAAGCTTCGTGACGCTTTTGGCTACGCAATACCCTCACAAAAAACAG
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                                                                                           gHisLeuPheGlyGlnLeuGluGlyAspArgPheProLeuLeuThrLysI
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3.804
80.511
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/translation="mtddmtkdwingcflorgiknrhigliaiggaigtgletigsgks
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/gene="ydgF"
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/gene="ydgf"
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/gene="ydgF"
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NIILGOETAEGSVWVSBANIGYLTQEVEDLPLEQTPEELFENETEKARGHVQNLMRH
LGFTAAQWTEPIKHMSMGERVKIKLMAYILEEKDVLILDEPTNHLDLPSREQLEETLS
QYSGTLLAVSHDRYFLEKTYNSKLVISNIGIEKQLWDVFSERNEREELRLKLETERQE
VLGKLSFMTPNDKGYKELDQAFNELTKRIKELDHQDKKD"
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QLSGGEKIKARLAKGLSEDADLLLIDETSHINJDEKSIOPILIQOLKHYNGTVILVSHDR
YFIJEAANTKIWSIEDGYTILEFKKONYSOZYMKPBEKKRITQDREYEKOOKWVERIEAOMN
GLASWSEKAHAQSTKKEGFKEYHRVKAKRTDAQIKSKOKRLEKELEKAKAEPVTPEYT
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/gene="expz"
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/db_xref="12632894"
/db_xref="SWISS-PROT:P39115"
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/protein_id="CAB12381.1"
/db_xref="GI:2632875"
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/note="similar to amino acid ABC transporter (permease)"
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                                                                                                                              Streptococcus mutans (strain:GS-5) DNA. Streptococcus mutans Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                          scrK gene for fruct
D16594
D16594.1 GI:451214
                                                                                                                                                                                                                                                                                                         STRPMI 1379 bp DNA BCT 04-FEB-1999 S.mutans pmi gene for mannosephosphate isomerase (complete cd gene for fructokinase (partial cds).
     Submitted (05-JUL-1993) to
                                                                                                          Streptococcus
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                                rect Submission
                                                                                  (bases 1 to 1379)
     the DDBJ/EMBL/GenBank
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Isolation, characterization and sequence analysis of the scrK gene encoding fructokinase of Streptococcus mutans
J. Gen. Microbiol. 139 (Pt 5), 921-927 (1993)
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Fax:043-279-2052)
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Genome Res. (2001) In press
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Direct Submission
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Lactococcus lactis subsp. lactis
Bacteria; Firmicutes; Bacillus/Clostridium group;
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/note="EVIDENCE BY HOMOLOGY BIO15.02 HYPOTHETICAL.
Conserved. 50% identical to PH1801 of Pyrococcus
horikoshii "
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'gene-"nush"

/note-"rutpence by HOMOLOGY BIOLL 02 RNA synthesis,

modification, and DNA transcription. COULD PARTICIPATES IN

BOTH THE TERMINATION AND ANTITERMINATION OF TRANSCRIPTION"
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alignment_block:
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Ratio:
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Gaps: 3
Percent Identity: 52.077
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US-09-462-846-2 x AE006310

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Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 uPheGlyGlnLeuGluGlyAspArgPheProLeuLeuThrLysIleLeuA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 MetTyrLysGlyPheThrLeuSerGluLeuTrpGluHisHisArgHisLe 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 ysTrpAlaPheAlaAlaHisGlnAsnGlyGlnSerValValGlnAsnGly 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 GluProLeuPhePheLysProValPheLysGluArgIleTrpGlyGlyTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spAlàAspGlnAspLeuSerValGlnValHisProAsnAspGluTyrAla 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rAlaLeuAlaAspPheGlyTyrThrIleProSerGlnArgThrGlyGluC 37
                                                                                                                                                                                                                                                                                   ArgArgValLysValLysProGlyAspPhePheTyrValProSerGlyTh 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eAspCysGlnLysAspAlaGluIleIleTyrGlyHisAsnAlaThrThrL 137
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yrProPheLysLysGlyAspHisMetLeuLeuProTyrGlyLeuGlyGlu 301
                                                                                                                                                CTGATACAACTTACCGTGTTTATGATTTCGACCGTAAAAATGACCAAGGA
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                                                                                                                                                                                                      ATGCAAAATTACAACTCTTGTGAAATCAAATTTCTTTGATGTTTATAAA
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                                                                                                                       TGGCAAATTCATGGTGACCATGAATTTACCAAAGTTGCTGATTACACTTT
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BASE COUNT
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VERSION
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LOCUS SPNEU1904 147006 bp
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US-09-462-846-2 x SPNEU1904
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                                                                                                                                                                                                                                                                     19 YThrAlaLeuAlaAsp...PheGlyTyrThrIleproSerGlnArgThrG
                                                                                                                                                                                                                                                                                                                                               79069 TCAGAACCATTATTTTTACAATCAGTTATGCAAGAAAAAATCTGGGGTGG
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                                                                                                                                                52 AsnGlyMetTyrLysGlyPheThrLeuSerGluLeuTrpGluHisHisAr 68
                                                                                                                                                                                                                  3 ThrGluProLeuPhePheLysProValPheLysGluArgIleTrpGlyGl
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                                                                                                              AATGGTCGTTACGAGGGAACAGATCTTGCTACTTTGTATGCGGAACACCG
leLeuAspAlaAspGlnAspLeuSerValGlnValHisProAsnAspGlu
                                          TGAATTATTTGGCAATCGTCCAGAACCTGTATTTCCACTTTTGACCAAGA
                                                                          gHisLeuPheGlyGlnLeuGluGlyAspArgPheProLeuLeuThrLysI 85
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Ratio:
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Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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Dopazo, J., Mendoza, A., Herrero, J., Caldara, F., Polissi, A.,
Humbert, Y., Friedli, L., Guerrier, M., Grand-Schenk, E., Gandi
Francesco, M., Buell, G., Feger, G., Garcia, E., Peitsch, M. and
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HTG; HTGS_PHASE2.
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3.467
76.582
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26837 c 3
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SEQUENCING IN PROGRESS ***,
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KEYWORDS
SOURCE
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AUTHORS
TITLE
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LOCUS AC027136
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Loh, P., Qi, S., Ray, L., Ford, B., Worrell, V., Iandolo, J. and Staphylococcus aureus BAC Clone sabac-106
Unpublished
2 (bases 1 to 4000-
                                                                         ACO27136.5 GI:8567822
HTG; HTGS_PHASE2; HTGS_DRAFT.
Staphylococcus aureus.
Staphylococcus aureus
Bacteria; Firmicutes; Bacillus/Glostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
1 (bases 1 to 49897)
                                                                                                                                                                                                                                                  AC027136 49897 bp DNA Staphylococcus aureus clone sabac-106,
                                                                                                                                                                                                                              ordered pieces.
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DRAFT SEQUENCE,
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Quality:
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US-09-462-846-2 x AC027136
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TITLE
JOURNAL
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                                         35973 ATAAACAGACGTTAATAGACATGATTGATAATCATGAATTTGACAGTCTT 36022
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                                                                                                                                                                                                                 103 AlaAsnIleHisGluAsnGlyGluLeuGlyLySThrGluCySTrpTyrIl 119
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ON Jun 15, 2000 this sequence version replaced gi:8225121.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 49897; contig of 49897 bp in length.
                                                                                                                elleaspCysGlnLysAspAlaGluIleIleTyrGlyHisAsnAlaThrT
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| ## TTTAGATGCAGCCCCAGGTGCTGAAATTATATATGGCGTACATGCACATA
  LeuArgArgValLysValLysProGlyAspPhePheTyrValProSerGl
                                                                                                                                                                                              GCTTTAAAACACGAA...GGCGAACTAGGTAAAACAGAATGTTGGTATAT 35922
                                                                                                                                                                                                                                                                         TAGATGCCAATGATAAATTATCTGTTCAAGTTCACCCAGATGATGACTAC
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                                                                           hrLysGluGluLeuThrThrMetIleGluArgGlyGluTrpAspGluLeu
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76.923
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9237 c 7267 g 17640 t
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AL520118 BG121340 AV551371 AW395401

18 AL520118 LTI\_NFL004 10 602351444F1 NIH\_MGC 71 AV551371 Arabidopsi 71 sh48f04.y1 Gm-c1017

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AUTHORS
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SOURCE
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                                                                                                 ATTCCGCGCTGCGCTGGAGCACAGCTATCGTCACGCCGCGCGGTGGATG
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Synechococcus elongatus.
Synechococcus elongatus
Bacteria; Cyanobacteria; Chroococcales;
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Cbases I to 561
Kerfeld,C.A., Tran,M.A. and Perry,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Cheryl Kerfeld
Molecular Biology Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Box 951570, Los Angeles, CA 90095-1570,
Tel: 310 825-6224
Fax: 310 206-3914
Email: kerfeld@mbi.ucla.edu
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Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ158357 655 bp DNA GSS 12-SEP nbxb0011003r CUGI Rice BAC Library Oryza sativa genomic nbxb0011003r, DNA sequence.
AQ158357 AQ158357.1 GI:3555382
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Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
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Clemson University
100 Jordan Hall, Clemson, SC 29634, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wing.R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Unpublished (1998)
Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 655)
/clone_lib="CUGIT Rice BAC Library"
/clone_lib="CUGIT Rice BAC Library"
/tissue_type="leaf"
/lab_host="E. coli DH10B"
/host="E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 398.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cultivar="Nipponbare"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa"
/strain="Japonica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson, SC 29634, USA
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                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                        SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est29:AL537077
                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
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US-09-462-846-2 x AQ158357
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 CysGln.LysAspAlaGluIleIleTyrGly...HisAsnAlaThrThrL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 TGCGCTGGCGTTTCCGTGACCGTTACCGAAGGGAATATCCTGTGCCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 .....LeuSerGluLeuTrpGluHisHisArgHisLeuPheGlyGln 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 GlnArgThrGlyGluCysTrpAlaPheAlaAlaHisGlnAsnGlyGlnSe 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 LysProValPheLysGluArgIleTrpGlyGlyThrAlaLeuAlaAspPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGAGGAACTTCCG......GGCCGGGGCGCTTGG 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ysGluGluLeuThrThrMetIleGluArgGlyGluTrp 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACGCCGCCGGCCGCGCGCAAGGACGAATGCTGGGTGATCCCTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isGluAsnGly...GluLeuGlyLysThrGluCysTrpTyrIleIleAsp 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGAGAAATTGTCGGTGCAGGTCCAACCGAACGATGAGCAGGCG.....C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pGlnAspLeuSerValGlnValHisProAsnAspGluTyrAlaAsnIleH 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGCCGGGCGATTCCACCCGGACCTGCTGATCAAGTATCTGTTCACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuGluGlyAspArgPhePro...LeuLeuThrLysIleLeuAspAlaAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGATCCGGTGGGCGAGGTCTGG......TTCCAG
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                                                                                                                                                                                                                                                                                                                                             AL537077 LTI_FL013_FBrn1 prime, mRNA sequence. AL537077
                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammelia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 830)
1 (bases 1 to 830)
1 (by Bases, C. Jessee, J. and Polayes, D.
1 (by Bases, C. Jessee, J. and Polayes, D.
1 (by Bases, C. Jessee, J. and Polayes, D.
1 (by Bases, C. Jessee, J. and Polayes, D.
2 (by Bases, C. Jessee, J. and Polayes, D.
3 (contact; Genoscope
                                                                                                                                                                                                                                                                                                                            AL537077.1 GI:12800570
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      Genoscope - Centre National de Sequencage
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Gaps: 11
Percent Identity: 32.317
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KEYWORDS SOURCE

COMMENT

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alignment_block:
US-09-462-846-2 x AL537077
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ORIGIN
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            131 GlyHisAsnAlaThrThrLysGluGluLeuThrThrMetIleGluArgGl 147
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                                                                                                                                                                                                           AAATGGGGGACAGGTATTTCTCAAGCCATGTTCCCATGTGGTATCTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rgPheProLeuIeuThrLysIleLeuAspAlaAspGln......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rGluLeuTrpGluHisHisArgHisLeuPheGlyGlnLeuGluGlyAspA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGCGGCGTCTCGTGGCCCAGCTGCATCTGCTGCAGAATCAAGCTATAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGCAGTGACTGTGGCCTTCACCAACGCTCGCGACTGCTTCCTCCACCTG
                                                                                                AACAAGTTGAGGTGGAACCCCTCTCAGCAGATGATTGGGAGATACTGGAG
                                                                                                                                                 lnLys.....AspAlaGluIleIleTyr
                                                                                                                                                                                                                                                              sGluAsnGlyGluLeuGlyLysThrGluCysTrpTyrIleIleAspCysG
                                                                                                                                                                                                                                                                                                                        GCTGAAATTAACAGACAAGTT......GGTCAAAAACTTGGACTCTC
                                                                                                                                                                                                                                                                                                                                                                     ...AspLeuSerValGlnValHisProAsnAspGluTyrAlaAsnIleHi 106
                                                                                                                                                                                                                                                                                                                                                                                                                            ATTTT.....AGTGATCAAGGTGAAAATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTCCCGGGTCCTTTGCGGCGCTAGGGTGGGCGAACCCAGAGCGACGCTC
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Email;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax : (1) 301 610 8371 Email : http://filipacth.com URL :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.50
0.760
49.398
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/dev_stage="pooled tissue from
week, 24 week and 26 week)"
/lab_host="DH10B"
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Gaps: 11
Percent Identity: 18.876
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LOCUS BF492790
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               BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 622 GAATACATTTTCAAAAGCTGATGCTGAATATAAAAAACTTCATAGTTATG 671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAACTGACACCAAACTCCTTATTCAGCCAAAGACACGCCGAGCCAAAGA 621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 675)

Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman, B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Park, S., Paragas, V., Phouanenavong, S., Wan, K., Yu, C., Celniker, S., Lewis, S. E. and Rubin, G.M.

Lewis, S. E. and Rubin, G.M.

Berkeley Drosophila Gene Collection Project

Unpublished (2000)

Other_ESTs: AT01206 3prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF492790 675 bp mRNA EST 06-DEC-2000 AT01206.5prime AT Drosophila melanogaster adult testes pOTB7 Drosophila melanogaster CDNA clone AT01206 5 similar to CG11661: FBan0011661 last_updated:000321, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu hit genomic sequence AE003525; hit genomic sequence AE003472 Plate: Ar.12 row: A column: 6 High quality sequence stop: 595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
Fax: 510 486 6798
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               134
               ω
/dev_stage="0-3 day old Ore-R males"
/lab_host="DH5-alpha or DH5-alpha TonA as per database (AT /lab_host="DH5-alpha or DH5-alpha TonA as per database (AT /lab_host="DH5-alpha or DH5-alpha TonA cells)"
21 on are in Tona cells)"
/note="Organ: ADUIT testes; Vector: pOTB7; Site_1: ECORI; /note="Organ: ADUIT testes; Vector: pOTB7; Site_1: ECORI; Site_2: Xho1; The mRNA for the testis library was made from testes and seminal vessicles hand dissected from 0-3 day old Ore-R males. RNA kindly provided by the lab of Margaret Fuller. Sized fractionated cDNAs were directly ligated into pOTB7. Plasmid cDNA library."

a 217 c 199 g 125 t
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                                                        KEYWORDS
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                      ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 LeuLeuThrThrLeuIleGluCysAlaTyr............Ph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 ArgGlyGluTrpAspGluLeuLeuArgArgValLysValLysProGlyAs 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 CATGTTCTCGACTCCTCCGCCGGCGGAGCACAAGTTCGAGACACACAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGGCTACTCCATGGCCAGTCCCAATGCTCTGGTCATGTGGGAAGGCCAG
                                                                                                                                                                                                                                          CACACAGCATGGAGGCATGGGCCCCGAGCACTCTTCCGGCCGCATTGAG
                                                                                                                                                                                                                                                                                                                                                                                          TTTGGGGACTTCTGCAACACGGCGCGCAGTGCATCATCGACACGTTCATAGC 526
                                                                                                                                                                                                                                                                           roTyr.......GlyLeuGlyGluPheLysLeuGluGlyTyrAlaGlu 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCCGTCTCCAACAGCTCCCTGTCGGAGTGTGCGGTCCTCGGCTTCGAGC 426
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Homo sapiens
                                                                          BE567646.1 GI:9811366
                                                                                                               mRNA sequence.
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alignment_block:
US-09-462-846-2 x BE567646/rev
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Quality:
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                                                                                     141 hrThrMetIleGlu.....ArgGlyGluTrpAspGluLeuLeuArgArg 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 AsnGlyGluLeuGlyLysThrGluCysTrpTyrIleIleAspCysGlnLy 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   833 TATAGAATAGGTCTGATGTGGCACCACCCC...,....TCATGAGA 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             745 GGGTCCCCCTTTAGTGTCTCCA..............CACGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 spLeuSerValGlnValHisProAsnAspGluTyrAlaAsnIleHisGlu 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 PheThrLeuSerGluLeuTrpGluHisHisArgHisLeuPheGlyGlnLe
CCGTTTTATTGGACCCAACAAAAGGAAATTGGGGAAAG...
                                                                                                                                                                                           A...AAGAAAATGCCCATAAGGCGTGGGGCCACCAATAATAACCAGGTTA
                                                                                                                                                                                                                                                                                      sAspAlaGluIleIleTyrGlyHisAsnAlaThrThrLysGluGluLeuT 141
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High quality sequence stop: 481.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 869)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/note="Organ: bladder; vector: pDNR-LIB (Clontech);
/note="Organ: blader; v
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/db_xref="taxon:9606"
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 hrThrTyrArgLeuTyrAspTyrAspArgLysAspAlaGluGlyLysLeu 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 salaileGlyLysGlyIleLeualaLeuGluThrGlnGlnAsnSerAspT 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 roPheLysLysGlyAspHisMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ432549 710 bp DNA GSS 03-OCT-:
1M0218G01F Mouse 10kb plasmid UUGC1M library Mus musculus
clone UUGC1M0218G01 F, DNA sequence.
                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0218 row: G column: 01
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 710.
                                                                                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                             84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                        plasmid inserts
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1 (bases 1 to 710)
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                                                                                                                                                                                                                                                                                                   308,
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  /organism="Mus musculus"
                                                  Location/Qualifiers
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seq_documentation_block:
LOCUS Ef489340 mRNA
DEFINITION AT25326.5prime AT Drosophila
Drosophila melanogaster cDNA
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ORIGIN
                                                                                                                  seq_name: gb_est88:BF489340
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FEATURES

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SOURCE KEYWORDS ACCESSION DEFINITION

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389

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429

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338 TGGGAGTGGGTCAGGCATAGAACAGGCCTAAGCAGTTACAAATGGCATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        538 GTAGCAGGTAGGATGACACAGAGCCTCAGTGCAGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 TrpAlaPheAlaAlaHisGlnAsnGlyGlnSerValValGlnAsnGlyMe
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                                                                                                                                                                                                                                                                                                                                                AGGCAAGCAACGTTCCAGAGATGGGGCAGGTAGGCACACACTGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0218G01"
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/sex="Male"
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melanogaster adult testes
clone AT25326 5 similar to
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06-DEC-2000 ult testes pOTB7 similar to CG7934:
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US-09-462-846-2 x BF489340
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AUTHORS
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    182
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    AAGGAGGGC......
                                                                      ...GluGlyLysLeuArgGluLeuHisLeuLysLysSerIleGluValIl 217
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                                                                                                                                                                    Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman, B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nuncoo, J., Pacleb, J., Park, S., Paragas, V., Phouanenavong, S., Wan, K., Yu, C., Celniker, S., Berkeley Drosophila Gene Collection Project Unpublished (2000)
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Mecazoa; Artropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophildae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence AE003325; hit genomic sequence AE003472
Plate: AT.253 zow: C column: 2
High quality sequence stop: 575.
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//dev_stage="0-3 day old Ore-R males"
//lab.host="hH5-alpha or hH5-alpha TonA as per database (AT
//lab.host="hH5-alpha or hH5-alpha TonA as per database (AT
//dev_stage="1" or has been contained by the lab of steel stage of the testis library was made
//dev_stage and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
//dev_stage of the lab of stage of the lab of lag of the lab of stage of the lab of stage of the lab of lag of lag of the lab of lag of lag of the lab of lag of lag
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/db_xref="taxon:7227"
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/sex-"male"
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LOCUS BE204501
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barrel medic.
Medicago truncatula
Medicago truncatula
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
                                                                                                                                                                                                                                                                                                                                            Texas A&M University
College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
Email: kate@mail.bio.tamu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VandenBosch, K., Endre, G., Hur, J., Moore, J., Beremand, P., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.
                                                                                                                                                                                               http://chrysie.tamu.edu/medicago
Seg primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                      Texas AsM University name:T264273e
TIGR sequence name:MTGAV89TK
More information is available at...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: VandenBosch K
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                                                                        /organism="Medicago truncatula"
|cultivar="genotype A17"
|/db_xref="taxon:3880"
|/clone="pKV0-16010"
/tissue_type="Seedling roots"
/dev_stage="Immediately prior to inoculation with
                                                      /clone_lib="KV0"
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                                                                                                                       DEFINITION
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LOCUS BF648628
                                                                                                                                                                                                               seq_name: gb_est90:BF648628
SOURCE
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                                                                                                       Br648628 592 bp
NF049H02EC1F1027 Elic
                                                                                  broads 592 bp mRNA EST 20-DEC-20 NF049H02EC1F1027 Elicited cell culture Medicago truncatula clone NF049H02EC 5', mRNA sequence.
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BF648628.1 GI:11913758
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/lab_host="E.coli strain XLOLR"
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uncatula cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uAspAlaAspGlnAspLeuSerValGlnValHisProAsnAspGluTyrA
                                                 TTGATAGCGAGACTGGAAAGAGCAAAGACAGCAGAGTGCGTACTAGCTCT
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                                                                                                                                                                                                                                                                                                                                      GAAATGATGATGAAGAAGGTAAGGGTGAACAGTGGGTTGAAGTTGTATCA
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ThrThrMetIleGluArgGlyGluTrpAspGluLeuLeuArgArgValLy
                                                                                          ... AspAlaGluIleIleTyrGlyHisAsnAlaThrThrLysGluGluLeu 140
                                                                                                                                                                                                                                      TGGGAGCCTAGAGCTTTTGTGTATCACAATTTTCTGACCAAGGAGGAATG
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
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The Samuel Roberts Noble Foundation
Of 73402, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: radixon@noble.org
Insert Length: 592 Std Error: 0.00
Plate: 049 row: H column: 02
Seg primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2510 Sam Noble Parkway, Ardmore,
Tel: 580 221 7302
Fax: 580 221 7380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Dixon RA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
4 hours after induction. Equal amounts of RNA from
each
time point were pooled and used for mRNA isolation."
a 121 c 132 g 166 t
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1.220
48.077
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/db_xref="taxon:3880"
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1. .592
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EST.
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                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence AE003325; hit genomic sequence AE003472
Plate: AT.120 row: G column: 10
High quality sequence stop: 598.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fruit fly.
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One Cyclotron Rd, Berkeley, CA 94720, USA
                     Ratio:
                                                                                                                                           137
                                                                                                                                           b
                                                                                                                                     /dev_stage "0-3 day old Ore-R males"
//dev_stage "0-3 day old Ore-R males"
//lab_host "DH5-alpha or DH5-alpha TonA as per database (AT
//lab_host "DH5-alpha or DH5-alpha TonA as per database (AT
121 on are in Tona cells)"
//note-"Organ: ADULT testes; Vector: pOTB7; Site_1: EcoRI;
//site_2: Xhol; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into pOTB7. Plasmid cDNA library."
a 212 c 192 g 127 t
91.50
0.984
48.187
                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                                                                           /clone_lib="AT Drosophila melanogaster adult testes pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                   /clone="AT12082"
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                                                                                                                              AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               589 CATAGCCAGCGGCGAAACCAAGTGGGTGCGCCAGTCTGGAGTCGTCATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 GluAspLeuLeuThrThrLeuIleGluCysAlaTyr......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                489 TCGAGCACGGCTACTCCATGGCCAGTCCCAATGCTCTGGTCATGTGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 lnGlnLysProPheLeuLeuIleSer.....ValIleGluGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 TGGCAACATGTTCTCGACTCCTCCGCCGCGGAGCACAAGTTCGAGACAC
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pgr491677 708 bp mRNA EST 06-DEC-2000 AT28475.5prime AT Drosophila melanogaster adult testes pOTB7 Drosophila melanogaster CDNA clone AT28475 5 similar to CG11661: FBan0011661 last_updated:000321, mRNA sequence.
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US-09-462-846-2 x BF491677
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JOURNAL
                                               413
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  247
                                                                                               234
                                                                                                                                            363
                                                                                                                                                                                                                                   325 TAAGGAGGGC.....ATCCACGTTCGACTATCCGGCCAGGATG 362
                                                                                                                                                                                                                                                                                                                                  275
                                                                                                                                                                                                                                                                                                                                                                            192 ArgLeuTyrAspTyrAspArgLysAspAla.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 lyLysGlyIleLeuAlaLeuGluThrGlnGlnAsnSerAspThrThrTyr 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 .GlyAspPhePheTyrValProSerGlyThrValHisAlaIle......G 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 CGCCTGAAACTGTGCCCCACTGGCATCAGCACGGACACCCTGAAGACGAT 174
                                                                                                                                                                                                                                                                                                                                                                                                                            225 ACAAGGGCATCCTTCGCATACTGGCCCAGCGCACGCAGATGGTGCAGGAC
                                                                                                                                                                                                                                                                                  202 ....GluGlyLysLeuArgGluLeuHisLeuLysLysSerIleGluValI 217
                                               GAGGACAAGGTGGTACAACTCACTGGACCACCTCTATCCCGACCAGGC
                                                                                         GluAspLeuLeuThrThrThrLeuIleGluCysAlaTyr......
                                                                                                                                                                                      leGluValProSerIleProGluArgHisThrValHisHisGluGlnIle 233
                                                                                                                                                                                                                                                                                                                                  TGGCAACATGTTCTCGACTCCTCCGCCGCCGGAGCACAAGTTCGAGACAC
....PheSerValGlyLysTrpAsnLeuSerGlySerAlaSerLeuLysG
                                                                                                                                         TGGAGCGCGCACCTTTTCGCACCGGCACCACGTCCTGCACCACCAGTCG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
Ratio:
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Berkeley Drosophila Gene Collection Project
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence AE003525; hit genomic sequence AE003472
Plate: AT 284 row: G column: 3
High quality sequence stop: 681.
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One Cyclotron Rd, Berkeley, CA 94720,
Fax: 510 486 6798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148
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Note="Organ: ADULT testes; Vector: pOTB7; Site_1: EcoRI; Site_2: Xhol; The mRNA for the testis library was made from testes and seminal vessicles hand dissected from 0-3 day old Ore-R males. RNA kindly provided by the lab of Margaret Fuller. Sized fractionated cDNAs were directly ligated into pOTB7. Plasmid cDNA library."
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48.187
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/db_xref="taxon:7227"
/clone="AT28475"
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'lab_host="DH5-alpha or DH5-alpha Tor
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AUTHORS
BASE COUNT
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGACAGTTTGGGGACTTCTGCAACACGGCGCAGTGCATCATCGACACGTT 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCTGCCACACACCATGGAGGGCATGGGC 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATAGCCAGCGGCGAAACCAAGTGGGTGCGCCAGTCCGGAGTCGTCATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGAGCACGGCTACTCCATGGCCAGTCCCAATGCTCTGGTCATGTGGGAA 562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, US
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est(
hit genomic sequence AE003472; hit genom
Plate: AT.246 row: C column: 5
High quality sequence stop: 585.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 652)

Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman, B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Park, S., Paragas, V., Phouanenavong, S., Wan, K., Yu, C., Celniker, S., Lewis, S. E. and Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF488952 652 bp mRNA EST 06-DEC-2000 AT24629.5prime AT Drosophila melanogaster adult testes pOTB7 Drosophila melanogaster cDNA clone AT24629 5 similar to CG11661: FBan0011661 last_updated:000321, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berkeley Drosophila Gene Collection Project Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fruit fly.
                          134
         /dev_stage="0-3 day old Ore-R males"
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//note="Organ: ADULT testes; Vector: pOTB7; Site_1: EcoRI; Site_2: Xhol; The mRNA for the testis library was made from testes and seminal vessicles hand dissected from 0-3 day old Ore-R males. RNA kindly provided by the lab of Margaret Fuller. Sized fractionated cDNAs were directly ligated into pOTB7. Plasmid cDNA library."
                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
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/clone="AT24629"
                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                                 /clone_lib="AT Drosophila melanogaster adult testes pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 652
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alignment\_scores:

Quality:

91

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Length:

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alignment_block:
US-09-462-846-2 x BF488952
                                                                                                                                       SOURCE
ORGANISM
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LOCUS BF638871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lyLysGlyIleLeuAlaLeuGluThrGlnGlnAsnSerAspThrThrTyr 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCAACATGTTCTCGACTCCTCCGCCGCCGGAGCACAAGTTCGAGACAC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .GlyAspPhePheTyrValProSerGlyThrValHisAlaIle.....G 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgValLysValLysPro......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leGluValProSerIleProGluArgHisThrValHisHisGluGlnIle 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ....PheSerValGlyLysTrpAsnLeuSerGlySerAlaSerLeuLysG
                                                                                                                                                                                                                                          BF638871 663 bp mRNA EST 19-DEC-2000 NF079F08PLIF1073 Phosphate starved leaf Medicago truncatula cDNA clone NF079F08PL 5', mRNA sequence.
Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., Way,G.D. and Harrison,M.J.
                                                              Medicago truncatula
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
                                                                                                                                                            EST.
barrel medic.
                                                                                                                                                                                                         BF638871.1 GI:11903029
                                             (bases 1 to 663)
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Percent Identity: 23.280
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: BF638871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-462-846-2 x BF638871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                         173 AATTTTGGGAAAGGACCAACCAAGAGGTTACTTAATGGGTTAAATGGTTT 222
                                                                                                                                                                                                                                                                                                                                    .ValLysProGlyAspPhePheTyrVal.....ProSerGlyThrValH 172
                         TTTTGTTGCATACGTAACACAAGAAGATGTGTTGTTAGGAACTCTTACAG
                                                              .....LysLeuArgGluLeuHisL 210
                                                                                                                 ATGACAGGAAATGTTTTTCTCAATGGGAAGAAAAAAACTCCAGGCTATGG
                                                                                                                                                         ThrThrTyrArgLeuTyrAspTyrAspArgLysAspAlaGluGly.....
                                                                                                                                                                                                         AATCCACTTTGCTTGATACACTTGCAGGTAGACTTGCAAAAAATGTGGTA 322
                                                                                                                                                                                                                                                 is \verb|AlaIleGlyLysGlyIleLeuAlaLeuGluThrGlnGlnAsnSerAsp|
                                                                                                                                                                                                                                                                                                 TGCTGAGCCTGGTAGAATCATGGCTATTATGGGTCCTTCTGGCTCTGGAA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                 .....ArgGlyGluTrpAspGluLeuLeuArgArgValLys..... 157
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Ratio:
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52.451
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132 isAsnAla......ThrThrLysGluGluLeuThrThrMetIleGlu 145
                                                                                                                                                   26 TCAAATCTACATAACAACATGGAGATTGAAGCAGCAAGTGGTAGCAACAA
TTAATAGAGGAAGTTTCTTAGCATGGGAAGATCTAAGAGTTATGTTGCCA 172
                                                                                                                    CAAAGGATACAACATGGAT...GAGAGTGATGAGGAAGCATATTGTGGCC 122
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402,
Tel: 580 221 7325
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate starved Leaf library Unpublished (2000)
Contact: Harrison MJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mjharrison@noble.org
Insert Length: 663 Std Error: 0.0
Plate: 079 row: F column: 08
Seq primer: TCACACAGGAAACAGGTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissuc_type="leaf"
/tissuc_type="leaf"
/dev_stage="trifoliate"
/dev_stage="trifoliate"
/note="Vector: Lambda Zap; At the trifoliate stage, M.
/note="Vector: Lambda Zap; At the trifoliate stage, M.
/note="Vector: Lambda Zap; At the phosphate rice wand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20uM potassium phosphate. RNA was prepared from above ground tissues."
a 107 c 157 g 180 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="NF079F08PL"
/clone_lib="Phosphate starved leaf"
/clone_lib="Phosphate starved leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Medicago truncatula"
/db_xref="taxon:3880"
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alignment_block:
US-09-462-846-2 x BE249341
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NF014C07LF1F1053 Developing leaf Medicago
NF014C07LF 5', mRNA sequence.
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1 (bases 1 to
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sp
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Fabales; Fabaceae; Papilionoideae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 580 24. ...
Email: gdmay@noble.org
Email
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402,
Tel: 580 221 7391
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
On Jul 13, 2000 this sequence version replaced gi:9119401.
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Plate: 014 row: C column: 07
Seg primer: TCACACAGGAAAAGCTATGAC.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Medicago truncatula"
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/clone_lib="Developing leaf"
/tissue_type="leaf"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of young, developing, mature and senescing leaves."
a 95 c 134 g 137 t
                                                                                                                                           89.00
1.290
47.260
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Gaps:
Percent Identity:
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KEYWORDS
SOURCE
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LOCUS BF493329
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 AGTGGGTTGAAGTTGTATCATGGGAGCCTAGAGCTTTTGTGTATCACAAT 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 712)

Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman, B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Park, S., Paragas, V., Phouanenavong, S., Wan, K., Yu, C., Celniker, S., Paragas, V., Phouanenavong, S., Wan, K., Yu, C., Celniker, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF493329 712 bp mRNA EST 06-DEC-2000 AT01657.5prime AT Drosophila melanogaster adult testes pCTB7 Drosophila melanogaster CDNA clone AT01657 5 similar to CG11661: FBan0011661 last_updated:000321, mRNA sequence.
                                                                                                                                                                                                                                   Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF493329
BF493329.1 GI:11576630
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berkeley Drosophila Gene Collection Project Unpublished (2000)
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence AE003472; hit genomic sequence AE003525
Plate: AT.16 row: E column: 9
High quality sequence stop: 479.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lewis, S.E. and Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fruit fly.
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JOURNAL COMMENT

TITLE'

alignment\_scores:

Quality:

Ratio: Percent Similarity:

BASE COUNT

165

FEATURES

source

Berman

REFERENCE AUTHORS

KEYWORDS SOURCE ORGANISM ACCESSION VERSION

EST

DEFINITION

524 GCCAGTTTGGGGACTTCTGCAACACGGCGCAGTGCATCATCGACACGTT 573  278 .MetlleSerGlyGluTyrValTyrProPheLysLysGlyAspHisMetL 294 :::	74 76	374 GAGGACAAGGTGGTGTACAACTCACTGGACCACCTTTATCCCGACCAGGC 423  247PheSerValGlyLysTrpAsnLeuSerGlySerAlaSerLeuLysG 262  :::      ::: :::      424 GCCCTACTCCGTCTTCAACAGCTCCCTGTCGGAGTGTGCGGTCCTTGGCT 473	7 leGluvalProSerIleProGluArgHisThrValHisHisGluGlnIle 23 ::    :::::::::::::::::::::::::::::::	AAAGTGGCGGACTGGTCGCTGGGCGGGCGTCGCCTCCCT GluGlyLysLeuArgGluLeuHisLeuLysLysSerIleGluVall	175 lyLysGlyIleLeuAlaLeuGluThrGlnGlnAsnSerAspThrThrTyr 191	161 .GlyAspPhePheTyrValProSerGlyThrValHisAlaIleG 175	155 ArgValLysPro	ign seg 1/1 to: BF493329	alignment_block: US-09-462-846-2 x BF493329	alignment_scores: Quality: 88.50 Length: 202 Ratio: 0.932 Gaps: 8 Percent Similarity: 47.030 Percent Identity: 23.762	/organism="prosophila melanogaster" /db_xref="taxon;7227" /clone="AT01657" /clone=lib="AT Drosophila melanogaster adult testes /clone_lib="AT Drosophila melanogaster adult testes /dev_stage="0-3 day old Ore-R males" /lab_host="0-3 day old Ore-R males" /lab_host="0-13 day old Ore-R males; vector; pOTB7; Site_1:

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Query length: 315
Database: Issued_s: 302621
Database sequences: 302621
Database length: 87301344
Search time (sec): 66.190000
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US-09-462-846-2
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Compugen Ltd.
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; LOCATION:
US-09-076-359-1
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                                                                                                          US-09-462-846-2 x US-09-076-359-1
                                                                                  Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1,
                                                                                                                                                                                                                                                                                                                                                             NAME: Gamson, Edwaru .

NAME: Gamson, Edwaru .

REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: PET1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 781-9470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    TELEFAX: (312) 781-9548 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
COMPUTER: LBM PC compatible
COMPUTER: DOS PC DOS/MS-DOS
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Gamson, Edward P
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                    468 TGGGGAAGTAAAACTGCGTTAACGGAACTTTATGGCATCGCCAATCCGCA
                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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31 rGlnArg...ThrGlyGluCysTrpAlaPheAlaAlaHisGlnAsnGlyG
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                  Quality:
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.cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-112-096-27
/cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-112-096-124
/cgn2_6/ptodata/1/ina/5A_COMB.seq:US-07-938-782A-1
/cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-630-524-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Truison, Anna J
APPLICANT: Green, Charles E
APPLICANT: Braun III, Carl J
TITLE OF INVENTION: CARBON-BASED PROCESS FOR SELECTION
TITLE OF INVENTION: TRANSGENIC PLANT CELLS
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Release #1.0, Version
                                                                                           Length: 382
Gaps: 21
Percent Identity: 20.157
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to: 1650
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alignment_block: US-09-462-846-2 x US-09-001-982-9 Align seg 1/1 to: US-09-001-982-9 from: 1 to: 3468	alignment_scores: Quality: 92.50 Ratio: 0.571 Percent Similarity: 47.929 Percent Identity: 18.639	NAME/KEY: CDS : LOCATION: 13468 US-09-001-992-9	DEDNESS: OGY: line E TYPE: C L SOURCE: ISM: Baci	FILEPHONE: 919-541-658/ FILEPAX: 919-541-6589 FINFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: FINCOTH: 3468 base pairs FIVER: BIGGER SACE	ENT INFORMANISS, J. Time ION NUMBER: /DOCKET NUM CATION INFOR	FILING DATE: US/09/001,962 FILING DATE: US/09/001,962 FILING DATE: US/08/602,737 FILING DATE: 21-FEB-1996	709  EADABLE FORM:  YPE: Floppy disk.  IBM PC compatib  SYSTEM: PC-DOS/  PatentIn Releas  PLICATION DATA:	APPLICANT: Bosch, Hendrick J.  APPLICANT: Stiekema, Willem J.  TITLE OF INVENTION: Hybrid Toxin  NUMBER OF SEQUENCES: 15  CORRESPONDENCE ADDRESS:  ADDRESSEE: NO. 6204246artis Corporation  STREET: 3054 Cornwallis Road  CITY: Research Triangle Park  STATE: NC  COUNTRY: USA	eq_documentation_block: eqequence 9, Application US/09001982 Patent No. 6204246 GENERAL INFORMATION:	267 uLeuIleSerValIleGluGlyGluGlyArgMetIleSerGlyGlu 282  ::::::::       ::: :::    ::::::::::	THE CO	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2388 ACTGGATGGGTTCGTGAAGAGTAGTCAAGATTTAGAAATTGATCTCATTC 2437
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                                                                                                                                                                               2920 ATGGACGCTCAAAATCTTGTCGCATCAATTTCAGATGTATATAGCGATGC 2969
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2999 AGATTTACACAGAGCTGTCCAATCGCTTACAACAAGCATCGTATCTGTAT 3048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154
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                                       232 lnIleGluAspLeuLeuThrThrLeuIleGluCysAlaTyrPhe... 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysAspAlaGluGlyLysLeuArgGluLeuHisLeuLysLysSerIleGl 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAAGTTCGAACAACCGATGGT.....TATGCGACGTTAGGAAATC 2719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gArgValLysValLysProGlyAspPhePheTyrValProSerGlyThrV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluGluLeuThrThrMetIleGluArgGlyGluTrpAspGluLeuLeuAr 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGATGGTAAATGCGCAACTG...GAAACAGAGCATCATCCTCATCCGATGG 2584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCTATCAAAAAGTAGATGCATCGGAGTTAAAGCCGTATACACGTTATAG 2387
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                                                                                                                                                                                                                                                                                                                                                                 CAAAGGGATAATACAAAATGGAGTGCAGAGCTAGGAAGAAAGCGTGCAGA 2819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGGATTTAAATTCGAGTGTAGACCAGGGAATCTGG.....GCGATCTT 2678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTGCTGTGAAGCAGCTCAAACACATGAGTTTTCTTCCTATATTGATACA 2634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         spCysGlnLysAspAlaGluIleIleTyrGlyHisAsnAlaThrThrLys 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....IleLeuAspAlaAspGlnAspLeuSerValGlnVal.... 96
                                                                                                                                 uValIleGluValProSerIleProGluArgHisThrValHisHisGluG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTACTGCAAATCCCTGGAATT
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ORGANISM: Gallid Herpesvirus; INDIVIDUAL ISOLATE: 632
US-08-156-866-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-156-866-1
                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                          alignment_scores:
   Quality:
                                                                                                                          Align seg 1/1
                                                                                                                                                                 US-09-462-846-2 x US-08-156-866-1
                                                                                                                                                                                                                       Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08156866 Patent No. 5443831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3065 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3149
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MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM/PC or Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPEFFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/156,866
FILING DATE: NO. 5443831 yet assigned CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/788,123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Keeler, Jr. Calvin L. APPLICANT: Poulsen, David J. TITLE OF INVENTION: Gene Encodin TITLE OF INVENTION: Infectious L NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 sTrpAsnLeuSerGlySerAlaSerLeuLysGln.....GlnLysProP 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248
                                                       548 GTTACTACGTGGGCATTATTCTCAAGACCCCAAATAACAAATGAGTACGT 597
                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
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COUNTRY:
                                                                            STREET: 1220 Mark
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Nucleic Acid
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pGlyGlyThrAlaLeuAlaAspPheGlyTyrThrIleProSerGlnArgT 34
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Y: U.S.A.
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Percent Identity: 19.437
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1195
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1321 TCATGTCCGTTCTGGGGACATCGAATACTATCTCGGTAGTGGCGGATTTC 1370
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                                                                                                                                                                     LeuLeuIleSerValIleGluGly.....
                                                                                                                                                                                                                                             AACCTTTTAACATCAGC...AGGCTTCATTTGGCTGAATGCGTTCCTACC 1270
                                                                                                                                                                                                                                                                                        .....TrpAsnLeuSerGlySerAlaSerLeuLysGlnGlnLysProPhe 266
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                                                        TATGACTATGACG......TTCTCGTCCGGAAAAC 1223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAGTTCGTGTTTCGTACAAAAACAGT...TACCACTTTTCACTTAAAGA 1194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTATCAAGTCAGGGATTTGGAAACCGGACAAATAAGACCCCCCTAAAAA 1047
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                                                                                                                      ATAGCCACGGAGGCCATAGATGGCATCTTTGCCAGAAAGTATAGTTCGAC
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117 788 674

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alignment_block:
US-09-462-846-2 x US-08-813-940-24
                                                                                                                                                                                                      ; LOCATION:
US-08-813-940-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-813-940-24
                                                                                        Percent Similarity:
Align seg 1/1 to: US-08-813-940-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3490
TELEPHONE: 2568-3499
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                 ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
ADDRESSEB: Woodcock Washburn Kurtz Mackiewicz & No. 5834279ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,271
FILING DATE: 07-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Methods of Identifying Compounds that TITLE OF INVENTION: Inhibit DNA Synthesis in Mycobacterium Tuberculosis and TITLE OF INVENTION: Composition, Reagents and Kits for Performing the Same NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rubin, Harvey
APPLICANT: Yang, Fude
APPLICANT: Avarbock, David
APPLICANT: Curran, Sean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 alTyrProPheLysLysGlyAspHisMetLeuLeuProTyrGlyLeuGly 300 :: ||||:::|||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 GluPheLysLeuGlu 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/813,940 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 19103
                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAATGTACCTAGAA 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24,
                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4, Application US/08813940 5834279
                                                                                                          Ratio:
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                                                                                                                                                                                                                     446..2620
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                                                                                      84.00
0.672
45.290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33,229
                                                                                        Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             UPAP-0220
 from: 1
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6
                                                                                        276
12
22.826
 4107
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_name	298 1882	282 1832	27 <sup>'</sup> 2 1782	255 1732	242 1691	225 1682	208 1633	192 1598	175 1563	158 1513	142 1475	128 1425	111 1375	96 13 <b>4</b> 6	84. 1296	67 1267	51.
: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-447-464-2	yLeuGlyGluPheLysLeuGluGlyTyr 307        ::::::::   :::       GCTAGGACAGATGAACCTGCACGGCTAC 1909	GluTyrValTyrProPheLysLysGlyAspHisMetLeuLeuProTyrGl 298 :::     :::::::   ::::: ### HIT	leGluGlyGluGlyArgMetIleSerGly	rGlySerAlaSerLeuLysGlnGlnLysProPheLeuLeuIleSerValI 272 :::: :::: :::::::::::::::::::::::::	IleGluCysAlaTyrPheSerValGlyLysTrpAsnLeuSe 255 :::    :::	rgHisThrValHisHisGluGlnIleGluAspLeuLeuThrThrThrLeu 241	UHISLEULYSLYSSETIleGluVallIeGluValProSerIleProGluA 225 :::    ::::::    :::::::    ::: CAACCTGTGCTCGGAGATCCTGCAAGTGTCTACGCCGTCATTGTTCAAC. 1681	ArgLeuTyrAspTyrAspArgLysAspAlaGluGlyLysLeuArgGluLe 208	lyLysGlyIleLeualaLeuGluThrGlnGlnAsnSerAspThrThrTyr 191	ILysProGlyAspPhePheTyrValProSerGlyThrValHisAlaIleG 175 :    :   caaggcacgggagTTCTTCCAGACGCTGGCCGAGCTGCAGTTCGAGTCCG 1562	ThrMetIleGluArgGlyGluTrpAspGluLeuLeuArgArgValLysVa 158    :::::     :::::  :: GAAATGGTCGATGACGCGCGCGCTCCGCAAGACCAAGAT 1512	leIleTyrGlyHisAsnAlaThrThrLysGluGluLeuThr 141 :::       :::        GGGTCTACGGTGGCGTTCGCTGACATCTCGGTCACCGAGAAGTACTAC 1474	uGlyLysThrGluCysTrpTyrIleIleAspCysGlnLysAspAlaGluI 128  :::     :::    	ValHisProAsnAspGluTyrAlaAsnIleHisGluAsnGlyGluLe 111	yslleLeuAspAlaAspGlnAspLeuSerValGln95    :::       ::: :::::::::::::::::::::	SATGHISLEUPHEGlYGInLEUGLUGIYASPATGPheProLeuLeuThrL 84	GlnAsnGlyMetTyrLysGlyPheThrLeuSerGluLeuTrpGluHisHi 67             CAGCTGGGCGCTCGTCAAGGTGCCGGCGGGGGTGTACCTGCACGCCCATCA 1266

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alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-462-846-2 x US-08-447-464-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION:
TELEPHONE: 212-790-9990
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5690 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-08-447-464-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION UMBER: US/08/447,464
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/130,570
FILING DATE: 01-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Schlessinger, Joseph
APPLICANT: Yan, Hai
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                   4091 TTTTCTCTACACAAGAATGGCTCTAGTGAGAAGCGTGAGGTACGACATTT 4140
                                                                                                                                         4170 TACCCGAG.....TACCCC.....ACACCCTTCCTGGCGTTTCTG 4204
                                                4205 CGCAGAGTCAAGACCTGCAACCCGCCTGACGCTGGCCCAGTTGTGGTCCA 4254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
106 sGluAsnGlyGluLeuGlyLysThrGluCysTrpTyrIleIleAspCys. 122
                                                                                                                                                                                  73 lnLeuGluGlyAspArgPheProLeuLeuThrLysIleLeuAspAlaAsp 89
                                                                                                                                                                                                                                                                  56 sGlyPheThrLeuSerGluLeuTrpGluHisHisArgHisLeuPheGlyG 73
                                                                                                                                                                                                                                                                                                                                                                          40 PheAlaAlaHisGlnAsnGlyGlnSerValValGlnAsnGlyMetTyrLy 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                           GlnAspLeuSerValGlnValHisProAsnAspGluTyrAlaAsnIleHi 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.00
0.778
51.185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 211
Gaps: 11
Percent Identity: 21.327
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Presson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Schlessinger, Joseph
APPLICANT: Yan, Hai
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 pAspGluLeuLeuArgArgValLysValLysProGlyAspPhePheTyrV 166
                                          REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 761
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1155 AVER CITY: New York STATE: New York COUNTRY: U.S.A. COUNTRY: U.S.A. ZIP: 10036-2711
TELEFAX: 212
TELEX: 66141
                                                                                                              NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrGlnGlnAsnSerAspThrThrTyrArg...LeuTyrAspTyrAspAr 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uGlnIleGluAspLeuLeuThrThrThrLeu 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTTCAAGAGGCTTGCCAGCT.....CCAAGGCACACACTTCGAGATTC 4582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gLysAspAlaGlu.GlyLysLeuArgGluLeuHisLeuLysLysSerIle 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alProSerGlyThrValHisAlaIleGlyLysGlyIleLeuAlaLeuGlu 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGCAGCGCGGGTGTGGGGGGCGTACTGGCTTCATTGTAATTGATGCCA 4304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCACTGCCAGCCTGCCTTGCAACAAGTTTA 4613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluValIleGluValProSerIleProGluArgHisThrValHisHisGl 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGCTGGCCCAGGTGGAGCCTGGCGAGCATGTCACAGGAATGGAGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....AATACCGAGGTCCCCGCGCGCAGCCTCTACACCTATATCCA 4488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AsnAlaThrThrLysGluGluLeuThrThrMetIleGluArgGlyGluTr 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Pennie & Edmonds
1155 Avenue of the Americas
                      212-869-8864/9741
                                                                                                                                                                                                          us/08/130,570
                                                                                                                                                                                                                                                                                                    US/08/716,679
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                                                                                                                                                                                                                                                                                                                                                    #1.25
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alignment_block:
US-09-462-846-2 x US-08-716-679-2
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; LOCATION:
US-08-716-679-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-716-679-2 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5690 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                        4448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4205
                                                                                                                                                  4489 GAAGCTGGCCCAGGTGGAGCCTGGCGAGCATGTCACAGGAATGGAGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: uni
MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4305 TGTTGGAGCGCATCAGAACAGAGAAGACGGTGGAT...GTGTACGGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4255 CTGCAGCGCGGGTGTGGGGCGTACTGGCTTGCTTCATTGTAATTGATGCCA 4304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4170 TACCCGAG.....TACCCC.....ACACCCTTCCTGGCGTTTCTG 4204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4091 TTTTCTCTACACAAGAATGGCTCTAGTGAGAAGCGTGAGGTACGACATTT 4140
                231 uGlnIleGluAspLeuLeuThrThrThrLeu 241
                                                                                                                                                                                                                                                                                                                                                               166 alProSerGlyThrValHisAlaIleGlyLysGlyIleLeuAlaLeuGlu 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                            149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 AsnAlaThrThrLysGluGluLeuThrThrMetIleGluArgGlyGluTr 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123
                                                                                                                                                                                       198 gLysAspAlaGlu.GlyLysLeuArgGluLeuHisLeuLysLysSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 sGluAsnGlyGluLeuGlyLysThrGluCysTrpTyrIleIleAspCys. 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 sGlyPheThrLeuSerGluLeuTrpGluHisHisArgHisLeuPheGlyG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 PheAlaAlaHisGlnAsnGlyGlnSerValValGlnAsnGlyMetTyrLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: unknown
                                                                                                        GluValIleGluValProSerIleProGluArgHisThrValHisHisGl
                                                                                                                                                                                                                                                                              ThrGlnGlnAsnSerAspThrThrTyrArg...LeuTyrAspTyrAspAr 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlnAspLeuSerValGlnValHisProAsnAspGluTyrAlaAsnIleHi 106
                                                              AGTTCAAGAGGCTTGCCAGCT.....CCAAGGCACACACTTCGAGATTC 4582
                                                                                                                                                                                                                                                                                                                        TCCACGAGGCACTGCTGGAGGCTGTGGGC.........
                                                                                                                                                                                                                                                                                                                                                                                                         paspGluLeuLeuArgArgValLysValLysProGlyAspPhePheTyrV 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCAGAGTCAAGACCTGCAACCCGCCTGACGCTGGCCCAGTTGTGGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InLeuGluGlyAspArgPheProLeuLeuThrLysIleLeuAspAlaAsp 89
                                                                                                                                                                                                                                        .....AATACCGAGGTCCCCGCGCGCAGCCTCTACACCTATATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ......GlnLysAspAlaGluIleIleTyrGlyHis 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
E: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
833..5338
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0.778
51.185
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Percent Identity: 21.327
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                                                                                                        231
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4583 ATCACTGCCAGCCTGCCTTGCAACAAGTTTA 4613

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; NAME/KEY: CDS; LOCATION: 8050..8052; OTHER INFORMATION: /note= "NNN=GCC, AGU, AGC, UCU, UCC, UCA, or UCG; OTHER INFORMATION: Xaa=Ala or Ser "
US-08-22-617A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFOMMATION:
REFERENCE/DOCKET NUMBER: 97,157
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11601 base pairs
TYPE: nucleic acid
cmn.aurenness. ginale
                                                                            alignment_block:
US-09-462-846-2 x US-08-222-617A-3/rev
                                                                                                                                                                              alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name; /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-222-617A-3
                                                                                                                                         Ratio:
Percent Similarity:
                                  Align seg 1/1 to reverse of: US-08-222-617A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DI
ORIGINAL SOURCE:
ORGANISM: Acres
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Van Liempt, Henk
APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
TITLE OF INVENTION: Quantities of ACV Synthetase
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
||I_CCATION: 388..11526|
||COTHER INFORMATION: /function= "Enzyme"
| OTHER INFORMATION: /product= "ACV Synthetase"
| FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
34 ThrGlyGluCysTrpAlaPheAlaAlaHisGlnAsnGlyGlnSerValVa 50
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STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08222617A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gutierrez, Santiago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Palissa, Harriet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acremonium chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
                                                                                                                                         84.00
0.503
47.042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                Length: 355
Gaps: 25
Percent Identity: 23.380
                                         from: 1
                                         to: 11601
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281	sProPheLeuLeuIleSerValIleGluGlyGluGlyArgMetIleSerG	264
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247 8362	luGlnIleGluAspLeuLeuThrThrThrLeuIleGluCysAlaTyrPhe:::::       :::       ::: aTGTCGTAGAATGCCTCGTGCGTGAGACCCTCCTC	231 8396
231 8397	lHisHis	228 8446
228 8447	IleGluValProSerIleProGluArgHisThrVa ::::::::::::::::::::::::::::::::::::	217 8496
216 8497	rgGluLeuHisLeuLysLysSerIleGluVal	206 8546
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192 8582	GlyIleLeuAlaLeuGluThrGÍnGlnAsnSerAspThrThrTyrAr	177 8625
176 8626	roGlyAspPhePheTyrValProSerGlyThrValHisAlaIleGlyLys         CCGGGGATCCCGTGGCAGAGTGCCTTGGTAAA	160 8657
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143 8708	AlaThrThrLysGluGluLeuThrThrMe	134 8757
133 8758	leaspCysGlnLysAspAlaGluIleIleTyrGlyHisAsn	120 8807
120 8808	nlleHisGluAsnGlyGluLeuGlyLysThrGluCysTrpTyrIleI ::::	104 8851
104 8852	SerValGlnValHisProAsnAspGluTyrAlaAs	93 8892
92 8893	euAspalaAspGlnAspLeu	86 8942
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72 8990	CCTTCGTGAATCGGAGCCATCCTCGTCATACTTGGGGATGACGGCAGCCT	9039
64 9040	lGlnAsnGlyMetTyrLysGlyPheThrLeuSerGluLeuTrp :::::::           ::: TCGCACACAGTTCCGGCGTTGAGCGTGTAGTAGCAGACGATGGCGCTGAC	50 9089
9090	ACGGGGGAAGGTTGGCGTGCAGGTGGTCACGGATACTCGATGCT	9133

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97,157
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 11.601 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 lyGluTyrValTyrProPheLysLysGlyAspHisMetLeuLeuProTyr 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Van Liempt, Henk
APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
TITLE OF INVENTION: Quantities of ACV Synthetase
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                  ORGANISM: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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OTHER INFORMATION: /note- "NNN-AGU, AGC, UCU, UCC, UCA, or UCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 300 Sout
CITY: Chicago
STATE: Illinois
                                                 NAME/KEY: CDS
LOCATION: 8050..8052
                                                                                                               NAME/KEY: CDS
LOCATION: 388..11526
OTHER INFORMATION: /function= "Enzyme"
OTHER INFORMATION: /product= "ACV Synthetase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCTCGCCGAAGTATCGCTCGATGAGGGAATTGCGCAGCTGGACTACGC 8207
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Garcia, Bruno D.
Gutierrez, Santiago
Barredo, Jose L.
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300 South Wacker Drive
                                                                                                                                                                                                                                                                                                           linear
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Palissa, Harriet
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231 8397	228 lhishis
228 8447	217IleGluValProSerIleProGluArgHisThrVa ::::::::::::::::::::::::::::::::::::
216 8497	206 rgGluLeuHisLeuLysLysSerIleGluVal
206 85 <b>47</b>	192 gLeuTyrAspTyrAspArgLysAspAlaGluGlyLysLeuA
192 8582	177 GlylleLeuAlaLeuGluThrGlnGlnAsnSerAspThrThTTyrAr     :::
176 8626	160 roglyAspPhePheTyrValProSerGlyThrValHisAlaTleGlyLys
160	143 tileGluargGlyGluTrpAspGluLeuLeuArgArgValLysValLysP ::::      ::: 8707 CGTTGAAAGGAACACGCTGAAGTCGGTCGTTCAGGACGTAGACGTGACTT
143 8708	134AlaThrThrLysGluGluLeuThrThrMe :::   :::::
133 8758	120 leaspCysGlnLysAspAlaGluTleIleTyrGlyHisAsn
120 8808	104 nIleHisGluAsnGlyGluLeuGlyLysThrGluCysTrpTyrIleI ::::    :::                 8851 TCTTGTAGAGTCTCTGGGGACGACTGTCACTTGCCTGTTTCGGC
104 8852	93SerValGlnValHisProAsnAspGluTyrAlaAs    ::::::
92 8893	86 euAspAlaAspGlnAspLeu
86 8943	73Gln.LeuGluGlyAspArgPheProLeuLeuThrLysTleL
72 8990	65
64 9040	50 lGlnasnGlyMetTyrLysGlyPheThrLeuSerGluLeuTrp :::::::     :::      9089 TCGCACACAGTTCCGGCGTTGAGCGTGTAGTAGCAGACGATGGCGCTGAC
50 9090	34 ThrGlyGluCysTrpAlaPheAlaAlaHisGlnAsnGlyGlnSerValVa                      9133 ACGGGGGAAGGTTGGCGTGCAGGTGGTCACGGATACTCGATGCT
to: 1160	Align seg 1/1 to reverse of: US-08-222-617A-24 from: 1 t
	alignment_block: US-09-462-846-2 x US-08-222-617A-24/rev
	Percent Similarity: 47.042 Percent Identity: 23.380

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
US-08-902-632-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
   Quality:
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US-09-462-846-2 x US-08-902-632-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-902-632-3 from: 1 to: 2325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1186 TTGTGGGAGAACATAGTGTACCTAGATTTTAGATCCCTGTACCCCTCAAT 1235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1377 GAGGCAGAAGATAAAGAAGAAGATGAAGGCCACGATTGACCCGATCGAGA 1426
                                                                                                                                                                                                                                       1673 AGAAGGCTATGGAGTTCCTCAACTATATCAACGCCAAACTTCCGGGCGCG 1722
                                                                                                                                                                                                                                                                                                                                                          1623 CGACGGATTTTTTGCCACAATACCTGGAGCCGATGCTGAAACCGTCAAAA 1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1540 ..ACGGCCTGGGGAAGGGAGTACATAACGATGACCATCAAG...... 1578
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1773 GAAGAAGTATGCGGTGATAGACGAGGAAGGCAAGATAACAACGCGCGGAC 1822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 s...TrpTyrIleIleAspCysGlnLysAspAlaGluIleIleTyrGlyH 132
                                                                                                                                                        132 isAsnAlaThrThrLysGluGluLeuThrThrMetIleGluArgGlyGlu 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 AspGluTyrAlaAsnIleHisGluAsnGlyGluLeuGlyLysThrGluCy 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 hrLysIleLeuAspAlaAspGlnAspLeuSerValGlnValHisProAsn 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 sHisArgHisLeuPheGlyGlnLeuGluGlyAspArgPheProLeuLeuT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 GlyMetTyrLysGlyPhe.....ThrLeuSerGluLeuTrpGluHi 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 ysTrpAlaPhe...AlaAlaHisGlnAsnGlyGlnSerValValGlnAsn 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 IleTrpGlyGlyThrAlaLeuAlaAspPheGlyTyrThrIleProSer..
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                                                                                                                     CTTGAGCTCGAGTACGAGGGCTTCTACAAACGCGGCTTCTTCGTCACGAA 1772
                                                                                                                                                                                                                                                                                                                                                                                                          .ProGlyAspPhePheTyrValProSerGlyThrValHisAlaIleGlyL 176
                                                                                                                                                                                                                                                                                       ys......GlyIle 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....GAGATAGAGGAAAAGTACGGCTTTAAGGTAATCTACAGCGACAC 1622
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0,532
                                                         .....GlnAsnSerAspThrThrTyrArgLeuT 194
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21
21,127
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COUNTRY USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATION SYSTEM: US/O8/834,306
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O8/834,306
FILING DATE: 15-APR-1997
CLASSIFICATION UMBER: US/O8/834,306
FILING DATE: 15-APR-1997
CLASSIFICATION UMBER: 31,392
REGISTRATION UMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.422C1
FELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2446 base pairs
TYDE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
; Sequence 17, Application US/08834306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2105 TCGTGCTCAAGGGCTCTGGGAGGATA.....GGCGACAGGGCGATACCG 2148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1823 TTGAGATTGTGAGGCGTGACTGGAGCGAGATAGCGAAAGAGACGCAGGCG 1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2064 GAGAGGAGTCAAAATA......CGCCCTGGAACGGTGATAAGCTACA 2104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 PheLysLysGlyAsp 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6300 COLUMCITY: Seattle
STATE: Washington
                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACTACAAGGCAACCGGTCCCCACGTTGCCGTTGCCAAGAGGTTGGCCGC 2063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGGTTCTTGAAGCTTTGCTAAAGGACGGTGACGTCGAGAAGGCCGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..ValileGluGlyGluGlyArgMetIleSerGlyGluTyrValTyrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rGlySerAlaSerLeuLysGlnGlnLysProPheLeuLeuIleSer.... 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....AlaGluGlyLysLeuArgGluLeuHisLeuLysLysSerIleGl 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leProGluArgHisThrValHisHisGluGlnIleGluAspLeuLeuThr 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reed, Steven G.
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOR THE DETECTION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PREVENTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-462-846-2 x US-08-834-306-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-834-306-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1727 GGGTCTCTCCCAAACAACAGTATTTCACACATCCAATTCCACGGGGA 1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1689 TACGTTAACGCGAGGAAGGCTTACTTTGGCACCTAC.....AA 1726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1678 ATTGGGAT.....TTC 1688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1664 ACAC.....GACACGGGCC 1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 roAsnAspGluTyralaAsnIleHisGluAsnGlyGluLeuGlyLysThr 114
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||||||:::::|||:::
1573 ATGGGAGGTGGATGACTGTAATTCATAGTGGCGGTAGACAAATACTTTCA 1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1526 GGAT...GACAATGACAAGACTGTGCTATTTGGTGTGTTTTACACCCATG 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1453 CTCTAGTGGTGATGGCGGTCATCCAC......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1407 .... CGAAGTGGACAGAATCAACCGTACCATTTCTTACACAAAACGTTCA 1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1850 AAGCATCTAAGATGGCTCATGGTCGGCGAGACAGGCCCAAAATACGATGA 1899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1623 ACAGGGTGG......GACCCAGAAAAACCGTGTCAGGTAGTGCTGCG 1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1479 ... GATAGGCCGAAGAAACGCACCCCCATTCCTTTGATTCGTGTGGTGAT 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 sGlyIleLeuAlaLeuGluThrGln...GlnAsnSerAspThrThrTyrA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 luTrpAspGluLeuLeuArgArgValLysValLysProGlyAspPhePhe 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 yHisAsnAlaThrThrLysGluGluLeuThrThrMetIleGluArgGlyG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 GluCysTrpTyrTleIleAspCysGlnLysAspAlaGluIleIleTyrGl 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 GlyAspArg......PheProLeuLeuThrLysIleLe 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 aHisGlnAsnGlyGlnSerValValGlnAsnGlyMetTyrLysGlyPheT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 uAspAlaAspGlnAspLeuSerVal......GlnValHisP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 hrLeuSerGluLeuTrpGluHisHisArgHisLeuPheGlyGlnLeuGlu 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 GlyTyrThrIleProSerGlnArgThrGlyGluCysTrpAlaPheAlaAl 42
                  TGGCAGCTCTTATTCTGCGAGTGCGTCCGAGGAAGGAAGCAGAGGTGGCA 1949
                                                                     euThrThrThrLeuIle.GluCysAlaTyrPheSerValGlyLysTrpAs
                                                                                                                                                                                                                                                                                                                                                                                                              rgLeuTyrAspTyrAspArgLysAspAlaGluGlyLysLeuArgGlu...
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                                                                                                                                                                                             oSerIleProGluArgHisThrValHisHisGluGlnIleGluAspLeuL 237
                                                                                                                                                                                                                                                   GCCATTTGTCACTCTTCAACGCCCGTTTGTATAACCGAAGACTCAATTCC
                                                                                                                                                                                                                                                                                                                                                                     GAGTG......GGGAAGTTGCAGAGTCCA 1799
                                                                                                                                                                                                                                                                                                         .....LeuHisLeuLysLysSerIleGluValIleGlu.....ValPr 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
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0.693
45.420
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Gaps: 15
Percent Identity: 20.992
                                                                           253
                                                                                                                                                                                                                                                      1849
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seq_documentation_block:
; Sequence 1, Application US/08032364
; Patent No. 5356623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY:
; LOCATION:
US-08-032-364-1
                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-462-846-2 x US-08-032-364-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-032-364-1 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 215-757-1590 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1950 GCTCCATGCCCGCGGGTACGTCCGAGGAAGGAAG 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/032,364
FILING DATE: 19330317
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION UMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 nLeuSerGlySerAlaSerLeuLysGlnGlnLys 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VON Tersch, Michael A.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CTYET1 TOXIN GENE
TITLE OF INVENTION: AND PROTEIN TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                              2352 ..ATAGATGAGTCAAAATTAAAAGCCTATACTCGCTATGAATTAAGAGGA 2399
                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                     49 alvalGlnAsnGlyMetTyrLysGlyPheThrLeuSerGluLeuTrpGlu 65
                                                                                                                                                                                                                                                  16 IleTrpGlyGlyThrAlaLeuAlaAspPheGlyTyrThrIleProSerGl 32
66 HisHisArgHisLeuPheGlyGlnLeuGluGlyAspArgPheProLeuLe 82
                                                                                                                                                                          32 nArgThrGlyGluCysTrpAlaPheAlaAlaHisGlnAsnGlyGlnSerV 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1601 Market Street, 36th Floor CITY: Philadelphia STATE: Pennsylvania COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3766 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Panit
ADDRESSEE: Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19103
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177..3689
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                                                                                                                                                                                                                                                                                                                                                                                                                        81.50
0.491
43.799
                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 379
Gaps: 20
Percent Identity: 18.734
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yGluTyrValTyrPro 286
253 n
240ThrLeuIleGluCysAlaTyrPheSerValGlyLysTrpAs 253 ::::::  :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   ::::   ::::   :::::   ::::::
230 isGluGlnIleGluAspLeuLeuThrThr
215GluvalIleGluValProSerIleProGluArgHisThrValHisH 230 :::    :::
204 LysLeuArgGluLeuHisLeuLysLysSerIle
187 eraspThrThrTyrArgLeuTyrAspTyrAspArgLysAspAlaGluGly 203    ::: :::                :::
179LeuAlaLeuGluThr
177 Glyīle
166 alProSerGlyThrValHisAlaIleGlyLys 176 :: ::    :::::::: 2713 CAAGATTAGGAAATCTGGAAGTTCATCGAAGAGAAACCATTAGTAGGAGAA 2762
149 pAspGluLeuLeuArgArgValLysValLysProGlyAspPhePheTyrV 166
134AlaThrThrLysGluGluLeuThrThrMetIleGluArgGlyGluTr 149 :::    :::    2643 GGATGCACAGACTTGCAAGAGGATTTAGGCGTGTG 2677
126 laGluIleIleTyrGlyHisAsn
116 STrpTyrIleIleAspCysGlnLysAspA 126
106HisGluAsnGlyGluLeuGlyLysThrGluCy 116
96 alHisProAsnAspGluTyrAlaAsnIle
82 uThrLysileLeuAspAlaAspGlnAspLeuSerValGlnV 96 :::::: :::         :::   2403AITGAAGATGTCAAGATCTAGAGGTTTATTTAATTCGTT 2442
2400 TAT

SArgHi 69	60LeuSerGluLeuTrpGluHisHisArgHi
	CTGGAAATACGAATTC
	59 hr
SlyPheT 59	42 aHisGlnAsnGlyGlnSerValValGlnAsnGlyMetTyrLysGlyPheT ::::::
eAlaAl 42 :: CTTATC 72	26 G1yTyrThrIleProSerGlnArgThrGlyGluCysTrpAlaPheAlaAl     :::::   ::::    23 GGTCAAGTCTTACCTGAAGAGACATCGGGAACGAAAGAGGGTGACTTATC
1879	Align seg 1/1 to: US-08-961-083-105 from: 1 to: 1
	lignment_block: US-09-462-846-2 x US-08-961-083-105
41 11 189	ty: 81.00 Length: 3 10: 0.570 Gaps: Lty: 41.642 Percent Identity: 17.8
Antigens and Vaccines	sequence 105, Application US/08961083 Patent No. 6199469 GENERAL INFORMATION: Streptococcus pneumoniae An NUMBER OF INVENTION: Streptococcus pneumoniae An NUMBER OF SEQUENCES: 452 CORRESPONDENCE ADDRESS: ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA ZIP: 20850 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb stora COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.30 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION NUMBER: US/08/961,083 PILING DATE: CLASSIFICATION: 435 PILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 36,373 REGISTRATION NUMBER: 36,373 REGISTRATION NUMBER: 98340P2 TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504 TELEPHONE: (301) 309-8504 TELEPHONE: (301) 309-8504 INFORMATION FOR SED ID NO: 105: SEQUENCE CHARACTERISTICS: LENGTH: 1879 base pairs TYPE: nucleic acid TYPE: nucleic acid TOPOLOGY: linear TS-08-961-083-105
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3245	3213 GGTCGTGGATACATCCTTCGTGTCACAGCGTAC

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292 875	275 uGlyArgMetIleSerGlyGluTyrValTyrProPheLysLysGlyAspH
275 852	259 SerLeulysGinGinLysProPheLeuLeuIleSerValIleGluGlyGl       
258	19
242	gHisThrValHisHisGluGlnIleGluAspLeuLeuThrThrThrI:::::       :::::::::::::::::::::::::
225 768	209 HisleulyslysSerIleGluValIleGluValProSerIleProGluAr
208 721	193LeuTyraspTyraspargLysaspalaGluGlyLysLeuargGluLeu
192 671	179 uAlaLeuGluThrGlnGlnAsnSerAspThrThrTyrArg
179 621	163 PhePheTyrValProSerGlyThrValHisAlaIleGlyLysGlyIleLe :::       572 TACTTCTATGAAGTAGACTTAAATGGCAATACTGTTGGTAAACAAGGTCA
571	2 CTGCTAAAAATCCTGCTTTACCTCCTCTTGAAGGATTAACAAAAGGGA
162	N
162 521	154 gArgValLysValLysProGlyAsp
154 471	144 IleGluArgGlyGluTrpAspGluLeuLeuAr 
143 421	127 lulleIleTyrGlyHisAsnAlaThrThrLysGluGluLeuThrThrMet
127 371	110 uLeuGlyLysThrGluCysTrpTyrIleIleAspCysGlnLysAspAlaG : : :         ::: 355 AGACAGCATGGTTC
110 354	94 ValGinValHisProAsnAspGluTyrAlaAsnIleHisGluAsnGlyGl ::::::::    :::::
93 304	86 euAspalaaspGlnaspLeuSer 
86 254	69 SLeuPheGlyGlnLeuGluGlyAspArgPheProLeuLeuThrLySlleL    :::::::           :::  221GAAGCTCAAAAAAATCCAGAGCTAACAGATGTCT
220	:::     :::    :::       :::       :::

	302 heLysLeuGluGlyTyrAlaGluCysTleValSerHis 314	
ъР 302 3081	285 rProPheLysLysGlyAspHisMetLeuLeuProTyrGlyLeuGlyGlu	
Ty 285 TG 3044	270 SerValIleGluGlyGluGlyArgMetIleSerGlyGluTyrValT	
Le 269 :: IC 2994	253 snLeuSerGlySerAlaSerLeuLysGlnGlnLysProPheLeuLeuIl   ::::::    ::::::::::::::::::::::::::	
DA 253 H 2944	242IleGluCysAlaTyrPheSerValGlyLysTrp	
. 241 3C 2894	230 HisGluGlnIleGluAspLeuLeuThrThrThrLeu	
s 229 T 2844	213 erileGluVallieGluValProSerileProGluArgHisThrValHis ::::    :::          2795 AGGCTTATCTTCCAGAACTACCTTTCATTCCAGGAATAAATGTGGTGATT	
S 213 : :G 2794	203 yLysLeu	
1 203 C 2744	187 SeraspThrThrTyrArgLeuTyrAspTyrAspArgLysAspAlaGluG:    ::::	
n 186 T 2694	179GlnGlnAsı	
. 178 G 2644	176 sGlyIle	
y 176 ; A 2594	166 ValProSerGlyThrValHisAlaIleGlyLy :::         ::::::::             ::: 2545 GCAAGATTAGGAAATCTGGAATTTATCGAAGAGAAACCATTAATTGGAGA	
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r 149     2509	134AlaThrThrLysGluGluLeuThrThrMetIleGluArgGlyGluT :::    :::    2475 TGGATGCACAGACTTGCAAGAGGATCTAGGCGTGT	
. 133 Г 2474	126 AlaGluileiletyrglyhisasn	
125	120IleAspCysGlnLysAsp :::      ::: :::    2375 GTGTGCCACACCTTGAATGGAATCCTGATTTAGATTGTTCCTGCAGAGAC	
119 2374	117 pTyrIle	
117	101 GluTyrAlaAsnIleHisGluAsnGlyGluLeuGlyLysThrGluCysTr     :::   ::: :::    2290 GAAACAGTAAATGTACCAGGTACGGGTTCCTTATG	

2239

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alignment_block:
US-09-462-846-2 x US-08-291-368-1
                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
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; CLONE: 81A2
US-08-291-368-1
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                                                                                                                                                                               Align seg 1/1
                                                                                                                                                                                                                                                                                                           Ratio:
Percent Similarity:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/597,607
EILING DATE: 15-0CT-90
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Sallwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA50.C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (904)375-8100
TELEPHANE: (904)372-8800
INFORMATION FOR SEQ ID NO: 1:
                                                                              2173 TTGTATCAAAAAATAGATGAGTCGAAATTAAAAGCCTATAACCGTTAC.. 2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NC
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Baci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: No. 5686069el Bacillus thuringiensis Isolates TITLE OF INVENTION: Active Against Lepidopteran Pests NUMBER OF SEQUENCES: 27 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN: aizawai
INDIVIDUAL ISOLATE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 3522 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Payne, Jewel M.
APPLICANT: Sick, August J.
                        70 uPheGlyGlnLeuGluGlyAspArgPheProLeuLeuThrLysIleLeuA 87
                                                                                                                            54 MetTyrLysGlyPheThrLeuSerGluLeuTrpGluHisHisArgHisLe 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 2421
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/291,368 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 32606
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                                                                                                                                                                                  to: US-08-291-368-1
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0.529
44.092
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Gaps:
Percent Identity:
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                                                                                                                                                                                                                                                                                                           2895 GAGAAATGTCATTAAAAATGGCGATTTCAATAATGGCTTATCATGCTGGA 2944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2545 GCAAGATTAGGAAATCTGGAATTTATCGAAGAGAAACCATTAATTGGAGA 2594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2475 TGGATGCACAGACTTGCAAGAG......GATCTAGGCGTGT 2509
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                                                285 rProPheLysLysGlyAspHisMetLeuLeuProTyrGlyLeuGlyGluP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 yLysLeu.....ArgGluLeuHisLeuLysLysS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 ValProSerGlyThrValHis......AlaIleGlyLy 176
                                                                                                                                               SerValIle...GluGlyGluGlyArgMetIleSerGlyGluTyrValTy 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGCTTATCTTCCAGAACTACCTTTCATTCCAGGAATAAATGTGGTGATT 2844
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TCCGGGGCGTGGCTATATCCTCCGTGTTACAGCGTAC...
                                                                                                      ACGTGAAAGGGCATGTAGATGTAGAACAAACAAACAACCACCGTTCGGTC
                                                                                                                                                                                                                                                     snLeuSerGlySerAlaSerLeuLysGlnGlnLysProPheLeuLeuIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                       HisGluGlnIleGluAspLeuLeuThrThrLeu.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAACATTGGTATGATTCATGCGGCAGATAGACTTGTTCATCAGATCCACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCACTGTCTCGTGTGAAGAGAGCGGAAAAAAAATGGAGAGACAAACGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGTGCCACACCTTGAATGGAATCCTGATTTAGATTGTTCCTGCAGAGAC
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                                                                                                                                                                                                                                                                                                                                                      ......IleGluCysAlaTyrPheSerValGlyLys.....TrpA 253
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241

229 2794 213 2744

2694

2644

178

2544

2424

2324

2894

3044

2994

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alignment_scores:
Quality:
Ratio:
Percent Similarity:
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                                        alignment_block:
US-09-462-846-2 x US-08-962-190-1
                                                                                                                                                                                                                   ; IMMEDIATE SOURCE:
; LIBRARY: Lambd
; CLONE: 81A2
US-08-962-190-1
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Align seg 1/1 to: US-08-962-190-1 from: 1 to: 3522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 15-OCT-90
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA50.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904)375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (904)375-8100
TELEFAX: (904)372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3522 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US
APPLICATION NUMBER: US
FILING DATE:
APPLICATION NUMBER: 0.
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringie
STRAIN: aizawai
INDIVLDUAL ISOLATE: PS81A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Payne, Jewel M.
APPLICANT: Sick, August J.
TITLE OF INVENTION: No. 5985267el Bacillus thuringiensis Isolates
TITLE OF INVENTION: Active Against Lepidopteran Pests
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 2421 N.W. CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32606
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2421 N.W. 41st Street, Suite A-1
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                                                                                        Length: 347
Gaps: 19
Percent Identity: 19.885
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285	SerValIleGluGlyGluGlyArgMetIleSerGlyGluTyrValTy	270
269 2994	snLeuSerGlySerAlaSerLeuLysGlnGlnLysProPheLeuLeuIle	253 2945
9 5	IleGluCysAlaTyrPheSerValGlyLysTrpA         :::       :::	242 2895
4 00	TATATGAT	230 2845
229 2844	erTleGluValIleGluValProSerIleProGluArgHisThrValHis::::::    :::::	213 2795
213 2794	YLYSLeuArgGluLeuHiSLeuLySLYSS ::::::         ::	203 2745
203 2744	SeraspThrThrTyrArgLeuTyrAspTyrAspArgLysAspAlaGluGl    ::: ::: ::: :::         :::    ::: GTGGATGCTTTATTCGTAGATTCTCAATATGATAGATTACAAGCAGATAC	187 2695
186 2694	LeualaLeuGluThr	179 · 2645
178 2644	SG1y11e	176 2595
176 2594	ValProSerGlyThrValHisAlaTleGlyLy :::    :::::::    :::::: GCAAGATTAGGAAATCTGGAATTTATCGAAGAGAAACCATTAATTGGAGA	166 2545
165 2544	rpAspGluLeuLeuArgArgValLysValLysProGlyAspPhePheTyr 	149 2510
149 2509		134 2475
133 2474	AlaGluIleIleTyrGlyHisAsn	126 2425
2424	GTGTGCCACACCTTGAATGGAATCCTGATTTAGATTGTTCCTGCAGAGAC	120 2375
2374	TCGAAAGTCCAATTGGAAGGTGTGGAGAACCGAATCGGT	5
117 2324 110	<pre>/rAlaAsnIleHisGluAsnGlyGluLeuGlyLysThrGluCysTr :::   :::   :::   ::: CAGTAAATGTACCAGGTACGGGTTCCTTATG</pre>	
100 2289	SPAlaAspGlnAspLeuSerValGlnValHisProAsnAsp: :: ::        :: :::::: ::: AAGATAGTCAAGACTTAGAAATCTATTTAATTCGCTACAATGCAAAACAC	87 2240
87 2239	uPheGlyGlnLeuGluGlyAspArgPheProLeuLeuThrLysIleLeuA(       :::   CAATTAAGAGGGTATATCG	70 2221
70 2220	MetTyrLysGlyPheThrLeuSerGluLeuTrpGluHisHisArgHisLe ; :::   :::    :::    :::   ::   ::   :::   :::   :::   :::   :::   :::   :	54 2173

2995	2995 CTTGTTGTCCCGGAATGGGAAGCAGAAGTGTCACAAACAA	3044
285	вGlyAspHisме	302
3045	3045 TCCGGGGCGTGGCTATATCCTCCGTGTTACAGCGTAC 3081	3081
302	302 heLysLeuGluGlyTyrAlaGluCysIleValSerHis 314	
3082	3082AAAGAGGGATATGGAGAAGGTTGCGTAACCATCCAT 3117	

Run

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                   Result,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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     110
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     945
311.8
258.4
258.6
225.8
225.8
225.8
275.2
37.2
34.4
                                                                                                                                                                                                                                                                                                                   Score
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## ALIGNMENTS

21-MAY-1999 (first entry)

X25733 standard;

DNA; 945 βÞ

Gram-positive bacterium with mutated or deleted gene for cysteine protease 1, 2 or 3 - used to express proteins with reduced proteolytic degradation, e.g. proteins, growth factors or enzymes Cysteine protease; Gram-positive bacteria; mutation; proteolysis; expression; heterologous protein; ss. B.subtilis cysteine protease CP1 coding sequence. WPI; 1999-132260/11. P-PSDB; W99371. Estell DA; 14-JUL-1998; 28-JAN-1999. W09904016-A2. Bacillus subtilis. 15-JUL-1997; (GEMV ) GENENCOR INT BV. 97EP-0305227. 98WO-US14529 deletion;

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Similarity

33.8%;

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                                                                                                                                                                                                                                                      Gram-positive bacterium with mutated or deleted gene for cysteine protease 1, 2 or 3 - used to express proteins with reduced proteolytic degradation, e.g. proteins, growth factors or enzymes
Sequence 945 BP; 290 A; 189 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cysteine protease; Gram-positive bacteria; mutiproteolysis; expression; heterologous protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gram-positive bacterium with mutated or deleted gene for cysteine protease 1, 2 or 3 - used to express proteins with reduced proteolytic degradation, e.g. proteins, growth factors or enzymes
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                             gattactatgccggagaaaacgaagagggagaactcggcaagacggaatgctggtacatt
                                             ccgcttctgacaaagctgctggatgtgaaggaagatacgtcaattaaagttcaccctgat
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use in vaccines for prevention infection. or attenuation of Enterococcus

Claim 1; Page 963-969; 2084pp; English

A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal infection. infection.

Sequence 12438 BP; 4071 A; 2218 Ç 2424 G; 3708 Τ; 17 other

DB 20;

Length 12438;

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RESULT
V52181/c
       The present invention describes a computer readable medium which has CC the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded CC on it, or a representative fragment or a sequence at least 95% identical CC to SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 CC to 391 (V52134 to V52524) are genomic fragments from Streptococcus CC pneumoniae. The present invention also describes an isolated nucleic acid CC molecule encoding a homologue of any of the fragments of the S. pneumoniae CC genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced CC by a process comprising: (a) screening a genomic DNA library using as a CC probe a target sequence defined by any of the sequences in SEQ ID NO:1 CC that hybridise to the target sequence and isolating the nucleic acid conclucies from the members; or (b) isolating mRNA, DNA or cDNA produced CC from an organism, amplifying nucleic acid molecules whose nucleotide CC sequence is homologous to amplification primers derived from the conclusion of the S. pneumoniae genome to prime the amplification and CC isolating the amplified sequences. The computer readable medium can be CC sequencts of the S. pneumoniae genome to prime the amplification modulating fragments of the S. pneumoniae genome. Products from the present CC invention can be used in diagnosis kits and assays, and pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGCCCATCCAAATGGAGTCTCTAAAGTTGCCAATGGTCGTTACGAGGGAACAGATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              totattocagaacggcatacagttoaccatgaacaaattgaggatttgcttacaacgaca
                                                                                                                                                                                                                                                                                                                                                 CTTGAAACCCAGCAGTCTAGCGATACCACCTATCGCGTCTATGACTTTGACCGCAAGGAT
                                                                                                                                                                                                                                                                                                                                                                ttggagacgcagcagaactcagacacacctacagattatatgattatgaccgaaaagat
                                                                                                                                                                                                                                                                                                                                                                                                                           ggggattttttctatgtgccaagcggtactgttcatgcgattggaaaaggaattcttgct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   actaccatgatagagcgtggagaatgggatgagctcttgcgccgtgtaaaggtaaagccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gattgccaaaaagatgccgagattatttatggccacaatgcaacaacaaaggaagaacta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTTATGGACTCGAGCATGAA---GGCGAACTCGGAAAAAACAGAATGCTGGTACATTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTTTGACCAAGATCCTCGATGCCAACGACTGGCTCAGTGTCCAAGTTCACCCAGACGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ctgcttacaaaatattagatgctgaccaggacttatctgttcaggtgcatccgaatgat 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTACTTTGTATGCGGAACACCGTGAATTATTTGGCAATCGTCCAGAACCTGTATTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agcgaattatgggaacatcacagacatttattcggacagcttgaaggggaccgtttccct 240
                                                                                                              GAAAAGACAGCTGACTACAGCTTATTGAGTGTCTTGGCTGGTCAAGGTCAGCTAACTGTT
                                                                                                                               aagcagcaaaaaccattccttcttatcagtgtgattgaaggggagggccgtatgatctct
                                                                                                                                                                                                                                                                                                         gcagaaggcaagctgcgcgagcttcatctgaaaaagagcattgaagtgatagaggtcccg
                                                                                                                                                                                                                                                                                                                                                                                                          CGCCAGCAAATCGAGGACAAGAACTGGGATGACTTGTTGACCAAAGTCCCTGTTAAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508;
                                                                                                                                                                                                                              GAGCCAGCAAATAGCCGTCCTGT---AACTGTTAAAGCAGATGATTTGCGTTCCACTCTC 1671
                                                                                                                                                                                                                                                                                        GACAAAGGCAACTTGCGTGAACTTCATCTTGAAAAATCCATCGATGTCTTGAACATTGGT
GCTTGGACTCTGGAAGGGCAAG
                          gaatttaaactcgaaggatatg
                                                       GACGGGAAAAATTATCCAATTCAAAAAGGCAGCCACTTTATCCTACCAAGTGATGTTGAA
                                                                               ggtgagtatgtctatcctttcaaaaaaggagatcatatgttgctgccttacggtcttgga
                                                                                                                                                                       CTTGTATCTAATGATTTCTTCGCAGTTTACAAGTGGGAAATTACTGGAAAAGTTGACTTT 1611
                                                                                                                                                                                               ttgattgaatgcgcttacttttcggtggggaaatggaacttatcaggatcagcaagctta
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Pred.
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No. 2.
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-62;
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RESULT
TRO389/c
ID TRO3
NX TRO3
AC TRO3
XX TRO3
AC Stap
XX Stap
XX Stap
XX Vacc
XX Stap
XX PD 28-A
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XX 26-F
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Best Local S
Matches 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a novel polypeptide, which is optionally expressed in NCIMB 40771. The polypeptide, and polynucleotide encoding it, are derived from Staphylococcus aureus. Cells expressing ligands binding the polypeptide can be used to isolated candidate compounds that bind and inhibit the activity of the polypeptide. Such compounds can be used as an immunogen to vaccinate an animal for protection against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus caused disease.
                                                                                                                                                                                                                                           556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus WCUH vaccine; disease; protectio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T80389
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                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                          acaaaaatattagatgctgaccaggacttatctgttcaggtgcatccgaatgatgatat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
CTTTGGTCACAACATCGTGAATTATTCGATAATGATTCACGAGATAGTTTCCCTCTGCTA
                                                                                                                                                                        ttatgggaacatcacagacatttattcggacagcttgaaggggaccgtttccctctgctt 246
                                                                                                                                                                                                                               CATCCAAATGGTCCTAATACAATTATCAATGGTCCATACAAGGATATGACCCTAGATCAA
                                                                                                                                                                                                                                                                                                                          AAAGCATTTAACTATGATATCCCTAATGAAACAACTGGTGAATGCTGGGCAATTTCTGCA 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                catcaaaatggtcaaagcgttgttcaaaacgggaatgtataaggggttcacgctcagcggaa 186
                                                                                                                                                                                                                                                                                                                                                                                                                   ACTATGGCATTATTTTTACAACCCGTTTTTAAAGACAGAATTTGGGGCGGTCATGCATTA
                                                ACTAAAGTATTAGATGCCAATGATAAATTATCTGTTCAAGTTCATCCAGATGATGACTAC
                                                                                                                                                                                                                                                                                                                                                       gctgattttggctataccattccgtcacaacgaacaggggagtgctgggcttttgccgcg 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1997-435166/40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 644 A; 428 C;
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he polypeptide(s) useful as anti-bact
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No. 6.3e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 644 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA sequence
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 misc_feature
                                                                         misc_feature
                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                               Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                   misc_feature
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                                                              CTTTGGTCACAACATCGTGAATTATTCGATAATGATTCACGAGATAGTTTCCCTCTGCTA
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                                                                                                               aatattagatgctgaccaggacttatctgttcaggtgcatccgaatgatgaatatgccaa
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                                                                                        AATAGTGGATGCAAGAGAATCACTTTCTATTCATGTGCACCCTGATAATTCTTATGCTTA
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RESULT
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                                                                                                          Barash SC,
Kunsch CA,
                                                     WPI; 1998-272225/24
                                                                                                                                                                                                                                                31-OCT-1996;
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                                                                                                                                                                                                                                                                                                         30-OCT-1997;
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                                                                                                                                                                                        (HUMA-) HUMAN GENOME
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                                                                                                       Choi GH,
Rosen CA;
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                                                                                                                                                                                           SCI INC
                                                                                                                                        Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; pharmaceutical composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S. pneumoniae; genome; diagnosis; assay; vaccine: pharmaceutical composition; ds.
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                                                                                                                                     Dougherty
                                                                                                                                        BA,
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                                                                                                                                        Fannon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 671
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Computer-readable medium with recorded Streptococcus pneumoniae

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F22305
ID F22305
XX F22305
AC F22305
XX 20-MAR
AX 20-MAR
XX Centro
XX Arabid
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pharmaceutical
18-MAR-1999;
01-APR-1999;
18-MAY-1999;
13-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13425 BP; 4434 A; 2362 C;
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                                                                                                                                                                                                                                                                                                                                                                                                              Centromere;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAR-2001
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                                                                                                                                                          17,-MAR-2000;
                                                                                                                                                                                                                         21-SEP-2000
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llarity 51.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              michrosome; vector; ds
                                                                                                                                                                                                                                                                                                                                                   thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                 2000WO-US07392
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                                    99US-0125219.
99US-0127409.
99US-0134770.
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Best Local S
Matches 77
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                                                                                                                                                                                                                                                                                                                                                              245208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1082138 BP; 348775 A; 194404 C; 195515 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant DNA construct comprising a plant centromere, producing stably inherited michrosomes which can serve as the construction of transgenic plant and animal cells
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                                                                                                                                                                                       Nitrite reductase molybdenum cofactor; MoeB; MoaB; MoaC; MoeA; MoaD; MobA; MoaB; MobB; MoaE; nitrate reduction; nitrite reduction;
                                                                                                                                                                                                                   S. carnosus
                                                                                                                                                                                                                                                                            T99451 standard;
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                   CDS
                                                                           CDS
                                                                                                                               Key
-35_signal
                                                                                                                                                            Staphylococcus
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                                                                                                                                                                                                                     nitrate reductase molybdenum cofactor
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                                                                                               5308 aacaaaccgcatctgattggatagatgtaagtagtgtagacgatgatacagaatggtata 5367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This DNA sequence from Staphylococcus carnosus includes genes that code for the nitrate reductase molybdenum cofactor blosynthesis proteins MoeB, MoaB, MoaC, MoeB, MoaD, MobA, MoaA, MobB and MoaE (see W26741-49). This gene region was identified following Tn917 insertion mutagenesis studies. Claimed DNA molecules (see T99449-51) can be used in the recombinant production of claimed proteins (see W26733-49) involved in nitrate and nitrite reduction in S. carnosus. These recombinant proteins, or cells expressing them, in free or immobilised form, can be used in a claimed method for reducing nitrate and nitrite in nitrate-polluted water, vegetables and other polluted materials.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 42-49; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant S. carnosus nitrate and nitrite reductase proteins - useful for reducing nitrate and nitrite in nitrate-polluted material
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                          353 acattattgattgccaaaagatgccgagattatttattggccacaatgcaacaaagg 412
                                                                                                                                                                                                                                                                                                                           Local Similarity
agaatattaattatccccaagatttagagagcataaagaaataataatcaacgtttaacg
                                                                                                                         cgaatgatgatatgccaacatacatgaaaacggtgagcttggaaaaacagaatgctggt 352
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                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                 The sequence is that of the cDNA encoding the human erythrocyte anion-transport protein (band 3). Nucleotides 1612-1662 (ANION 1) or 2434-2481 (COOH) of this sequence encode a peptide which is immunore reactive with antibodies to senescent cell antigen (SCA). The antigen and peptides can be used in any method or technique involving or requiring the inhibition of the binding of senescent cell igG to senescent cells in vitro or in vivo. The prods. can be used in to examine various physiological, biochemical, and immunological mechanisms in humans and other animals, such as those relating to cellular ageing, degeneration, and life span; removal of senescent cells; anion transport across cellular membranes; disease cellular ageing, degeneration, and life span; removal of senescent cells; anion transport across cellular membranes; disease to thrombocytopenia purpura; other autoimmune disease mechanisms, such as rheumatoid arthritis and systemic lupus crythematosus; and other diseases such as those involved in malata and cancer. More
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic senescent cell antigen and peptide(s) - used to detect antibodies to SCA, study cellular ageing and auto-immune mechanisms, separate anions and treat auto-immune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q15172 standard; cDNA; 3475 BP
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                                                                                                                                       specifically, the prods. are useful in cosmetic and pharmaceutical compsns., diagnostic kits, and methods for detecting or measuring hbs to SCA, studying cellular ageing and autoimmune mechanisms,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAY-1990;
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                                                                       SCA, studying cellular ageing and autoimmune mechanisms, ting anions from a gas or liquid, or diagnosis and treatment of the diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R15355
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Query Match
Best Local Sim
Matches 80;

Similarity 50.6 80; Conservative

0;

3,5%;

Score 33.2; Pred. No. 3; Mismatches

В

12; 78;

Length Indels

3475; 0;

Gaps

0

Sequence

3475

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672

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1050 C;

997

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756

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11-MAR-1998
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31-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09946281-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO1012 nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tatggccacaatgcaacaacaaggaagaactaactac 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gagcttggaaaaacagaatgctggtacattattgattgccaaaaagatgccgagattatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caggaccacgccatggaggagctgcaggatgattatgaagacatgatggaggagaatctg 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
          98US-0078886.
98US-0078910.
98US-0078939.
98US-0079556.
98US-0079663.
98US-0079728.
98US-0079728.
98US-0079728.
98US-0079728.
98US-0079728.
98US-0079728.
98US-0080165.
98US-0080165.
98US-0080165.
98US-0080177.
98US-0080178.
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98US-0081195.
98US-0081195.
98US-0081179.
98US-00811817.
98US-00811817.
98US-0081195.
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          22-APR-1998
23-APR-1998
23-APR-1998
24-APR-1998
29-APR-1998
30-APR-1998
30-APR-1998
30-APR-1998
30-APR-1998
30-APR-1998
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31-APR-1998
31-APR
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21-APR-1998;
22-APR-1998;
22-APR-1998;
The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. Z33891 to 234338, and Y41685 to Y41774 represent polynucleotide and polypeptide
                                                                                                                                                                                                                                                                                               New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -  \frac{1}{2} \int_{-\infty}^{\infty} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wood
                                                                                                                                                                                                                                                        Claim
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DB; Y41758.
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98US-0083767
98US-0083796
98US-0083325
98US-0083495
98US-0083554
98US-0083554
98US-0083554
98US-0083654
98US-008466
98US-008466
98US-008466
98US-0084637
98US-0084637
98US-0084637
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98US-0084637
98US-0085333
98US-0086577
98US-0085573
98US-0085573
98US-0085573
98US-0086614
98US-0086570
98US-00866392
98US-0086414
98US-0086692
98US-0086416
98US-0086416
98US-0086416
98US-0086416
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98US-0082569.
98US-0082700.
98US-0082704.
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RESULT 14
C78573
ID C78573
XX C78573
AC C78573
AC C78573
XX 08-FEB
XX Human;
KW Expres
OS Homo s
XX W02000
YN W02000
YN W02000
YN W02000
YN W02000
YN W02000
PD 14-SEP
PF 18-FEB
XX 08-MAK
PR 12-MAK
PR 02-UNI
PR 23-UID
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
Ashkenazi AJ, Baker KP,
Ferrara N, Filvaroff E,
Goddard A, Godowski PJ,
Kljavin IJ, Kuo SS, Napi
Shelton DL, Stewart TA,
                                                                                                                                                                    30-NOV-1999;
02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
30-DEC-1999;
30-DEC-1999;
05-JAN-2000;
06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted protein; transmemb: expressed sequence tag; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C78573 standard; cDNA; 4040
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                                                                                                                                                                                                                                                                                                                         26-JUL-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                  28-APR-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-1999;
12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO1012 (UNQ495) nucleotide sequence SEQ ID NO:458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                  (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                 23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266
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mes 96; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gcgattttttaaaaataaatagagcatatgaagtactcaaagatgaagatctacggaaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        attrattcggacagcttgaagggaccgtttccctctgcttacaaaaatattagatgctg 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4040 BP; 1269 A; 702 C; 832 G; 1237 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           given
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milarity 47.8%;
Conservative
                                                                                                                                                    ; 2000WO-US00219.
; 2000WO-US00277.
; 2000WO-US00376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000WO-US04341
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99WO-US28551.
99WO-US28565.
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                                                                                                                                                                                                             99WO-US31274
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99WO-US31243
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99US-0162506
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99US-0123957
                                                                                                                                                                                                                                                                                                                                                               99US-0141037
                                                                                                                                                                                                                                                                                                                                                                                    99US-0134287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the exemplification of the present invention.
KP, Botstein D, Desnoyers L, Eaton DL;
E, Fong S, Gao W, Gerber H, Gerritsen
PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
Napier MA, Pan J, Paoni NF, Roy MA;
TA, Tumas D, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane protein; detection; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Length 4040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO; EST; cytostatic;
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Best Local
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(HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    c78458 to c78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bloactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bloactive molecules to cells. C78600 to C78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
                                                                                                       05-NOV-1998;
                                                                                                                                                                                                                            WO200025728-A2
                                                                                                                                                                                                                                                                    Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                          plasmodium falciparum; chromosome 2; human malaria parasite;
antimalarial; malaria; protozoacide; infection; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                      07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A70106 standard; DNA; 7458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Fig 189; 636pp;
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                                                                                                                                               05-NOV-1999;
                                                                                                                                                                                       11-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum chromosome 2 related DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4040 BP; 1269 A; 702 C; 832 G; 1237 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      687 agtatgacaaatatggagaaa 707
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Similarity 47.8%;
96; Conservative
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                                                                                                                                               99WO-US26796
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. CC Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II). CC (I) and (II) are useful for the development of vaccines against CC (I) and (II) are useful for the development of vaccines against CC antibody raised to immunogens comprising the sequences of (I) are CC (I) (especially when they are rifins or secreted or membrane proteins) CC can aid the identification of infection with P. falciparum. Furthermore, CC (II) (especially when they are rifins or secreted or membrane proteins) CC can aid the identification of drugs to treat or prevent P. falciparum CC p. falciparum. Sequencing of the Plasmodium chromosome 2 and the complexity of the parasition of proteins encoded by it will help to expand CC our understanding of parasite biology, a process hampered by the CC complexity of the parasitic lifecycle, and provide new targets for CC resistance to insecticides have led to a resurgence of malaria in many CC parts of the world, and there is a pressing need for vaccines and new CC drugs. A70078 to A70287 and B18144 to B18352 represent nucleotide and CC protein sequences given in the present invention, but which are not expecifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins encoded by chromosome 2 of the human
plasmodium falciparum, useful as antimalarial
diagnosis of P.falciparum infection -
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Sequence 7458 BP; 3523 A; 514 C; 1174 G; 2247 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 462-464; 577pp; English.
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δÃ δÃ Qy 밁 멍 밁 Query Match 3.5%; Score 33; DB 21; Length 7458; Best Local Similarity 49.2%; Pred. No. 5.3; Matches 6000 318 258 agatgctgaccaggacttatctgttcaggtgcatccgaatgatgaataatgccaaccataca 317 87; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Search completed: May 17, 2001, 15:41:11 Job time: 3232 sec

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IMMEDIATE SOURCE:
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Sequence 6,	Sequence 5,	Sequence 5,	Sequence 1,	Sequence 1,	Sequence 18	Sequence 2,	Sequence 18	Sequence 1,									
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 2/21
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: SCHEIFLINEER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)683-4109
TELEX: 899149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1800 Dia
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road,
                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DORNER, F.
SCHEIFLINGER, F.
SCHEIFLINGER, F.
G.
                                                                                                                           7218 base pairs
                                                             linear
                                                                                 single
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RESULT 2
US-08-964-268-19/c
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                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WEI, YING-FEI
APPLICANT: RUBEN, STEVEN M
APPLICANT: SANCAR, AZIZ
APPLICANT: HSU, SHIAO-WEN D
APPLICANT: KAZANTSEV, ALEKSEY G
TITLE OF INVENTION: HUMAN BLUE-LIGHT PHOTORECEPTOR hCRY2
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                      NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0750001/EKS
TELECOMMUNICATION INFORMATION:
                                                                                                                                        FILING DATE: HEREWITH
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,189
FILING DATE: 04-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1092
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                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1100 NEW CITY: WASHINGTON
                                                                        TELEPHONE:
                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/964,268
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                                                            202-371-2540
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                                                                          202-371-2600
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US-08-894-731-1
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; MOLECULE TYPE:
US-08-964-268-19
                                                Sequence 1, Application US/08477451
Patent NO. 5928865
GENERAL INFORMATION:
APPLICANT: Covacci, Antonello
TITLE OF INVENTION: Helicobacte
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.2%;
Best Local Similarity 49.7%;
Matches 78; Conservative
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
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Best Local Similarity 47.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MINE, TOShiki
APPLICANT: OHYAMA, Akio
APPLICANT: HIYOSHI, TOTU
APPLICANT: KASAOKA, Keisuke
TITLE OF INVENTION: COLD-INDUCIBLE PROMOTER SEQUENCE
ETLE REFERENCE: 760-234P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/08/894,731 CURRENT FILING DATE: 1997-10-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 36
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Solanum tuberosum
                 NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                       276
                                                                                                                                                                                                                    336 aaaaacagaatgctggtacattattgattgccaaaaa
                                                                                                                                                                                                                                                                                                                              156 aaaaattgttgtgtactattttgatttattgagaaaacgaatcattgttgtatagggtaa 215
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     ADDRESSEE:
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STRANDEDNESS: singl
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Corporation
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                                                Pylori Cagi Region
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

94608-2916

USA

CA

STREET: 4560 Horton Street CITY: Emeryville

NAME:

McClung, Barbara G.

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; MOLECULE TYPE: US-08-477-451-1
                                                                                                                                                                                                                                                                                                                                                         US-08-477-451-5/c
; Sequence 5, Application US/08477451
; Patent No. 5928865
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Best Local Similarity
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TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0335
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510.601-2708
                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4195 TTTTGCTCGGCAACTGACATCATTCAGGAATAGTAAACCTACTTGTCCCCAACCATTTTTC 4254
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
| COMPUTER: IBM PC compatible
| COMPUTER: PC-DOS/MS-DOS
| SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                     APPLICANT: Covacci, Antonello TITLE OF INVENTION: Helicobact
                                                                                                                                                                                                                                                                                                                                                                                                                                                               4315 TCA 4317
                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    800 ttottatcagtgtgattgaaggggagggccgtatgatctctggtgagtatgtctatcctt 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              740 tttcggtggggaaatggaacttatcaggatcagcaagcttaaagcagcaaaaaccattcc 799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
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                                                                                                                                                                                                     CITY: Emeryville STATE: CA
                                                                                                                                                                                                                                     STREET:
                                FILING DATE:
              CLASSIFICATION:
                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                      ADDRESSEE:
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nucles: single
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                                                                                                                                                                                                 CA
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                                                                                                                                                                                   USA
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                                                                                 PatentIn Release #1.0, Version #1.30
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                         07-JUN-1995
INFORMATION:
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                                                                                                                                                                                                                                                                                                          Helicobacter Pylori Cagi Region
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Pred. No. 16;
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-477-451-5
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                             TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Covacci, Antonello TITLE OF INVENTION: Helicobact NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             740 tttcggtggggaaatgggaacttatcaggatcagcaagcttaaagcagcagaaaaaccattcc 799
TOPOLOGY: 1
MOLECULE TYPE:
                                            SEQUENCE CHARACTERISTICS:
LENGTH: 19932 base pairs
TYPE: nucleic acid
                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                       TELEPHONE:
                                                                                                                                                        REGISTRATION NUMBER: 33 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 07-JUN
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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                            STRANDEDNESS:
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                                                                                                                            510-601-2708
                                                                                                                                                                                                                                   UMBER: US/08/477,451
07-JUN-1995
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DNA (genomic)
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Pred. No. 16;
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Patent No. 6103893
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/GB95/
FILING DATE: 22.03.95
ATTORNEY/AGENT INFORMATION:
NAME: Anita E.Nador
REGISTRATION NUMBER: 1557
REFERENCE/DOCKET NUMBER: 1557
TELECOMBUNICATION INFORMATION:
TELEPHONE: (416) 368-2400
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                                                    FRAGMENT TYPE:
ORIGINAL SOURCE: clor
ORGANISM: Solanum t
STRAIN: Cv desiree
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                    TELEFAX: (416) 363-7246 INFORMATION FOR SEQ ID NO:
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                                                                                                                                              DESCRIPTION:
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WORD 7.0 for Windows CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,
FILING DATE: FILED CONCURRENTLY
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: IMB 1.44 MB High Density Diskette
COMPUTER: COMPAQ Deskpro 590 (IBM PC compatible)
OPERATING SYSTEM: MINDOWS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: National Starch and Chemical Investment
APPLICANT: Holding Corporation
TITLE OF INVENTION: Method for Producing Altered Starch
TITLE OF INVENTION: from Potato Plants
                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 3128 base pair
                                                                                                                                                                                                       MOLECULE TYPE:
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                                                                                                                                                                                                                                         LENGTH: 3128 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Toronto
STATE: Canada
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TISSUE TYPE:
                    HAPLOTYPE:
                                  DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                             TOPOLOGY:
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Box 194, 24th Floor, Toronto-Dominion Bank Tower
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                                                                                                                                                                                    cDNA encoding starch branching enzyme
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52.8%;
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                                    mature tuber
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Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: 3.5 DI
MEDIUM TYPE: storage
                                                                                                                                                                                                                        SOFTWARE: Word Perfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL TITLE OF INVENTION: TARGET GENES NUMBER OF SEQUENCES: 111
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IMMEDIATE SOURCE:
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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STREET: Suite 4700
CITY: Los Angeles
STATE: California
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OPERATING SYSTEM: IBM F.C.
OPERATING SYSTEM: IBM F.C.
OPERATING DATA:
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CLONE: 1.2.1 and E2
                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: Septem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHROMOSOME/SEGMENT:
                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  RY: U.S.A.
90071-2066
                                                Warburg, Richard J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08714918
                                                                                                                                                                                                                                                                                                                                                                                                                                    633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sun, Dongxu
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                                                                                    September 15, 1995
                                                                                                                                                                                     September 13, 1996
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                                                                                                                                                                                                                                                                                                              Diskette,
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DD: branching enzymes
complements KV832 E. coli glycogen
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Pred. No. 1
             222/005
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TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                             SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,31
FILING DATE: WARCH 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/09,102
ENTIME TARKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Schmid, M
APPLICANT: Sun, Dong
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No.
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
          REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 agcgttgttcaaaaocggaatgtataaggggttcacgctcagcgaattatgggaacatcac 201
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                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                            NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327
                                                                                                                 FILING DATE: December APPLICATION NUMBER: FILING DATE: Septer
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                               90071-2066
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6187541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Martin, Patrick K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schmid, Molly B.
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Malouin, Francois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lyon & Lyon
                                                                                                                                December 22, 1995
UMBER: 60/003,798
                                                                                                                 September 15, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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955-0440
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51.78;
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                                                                                                                                                                                                                                                                                                                          IBM P.C.
                                                                                                                                                                                                                                                                       us/09/265,315
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                                               240/247
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Pred. No. 10;
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Best Local Similarity
Matches 62; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-265-315-83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                  APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY,AGENT INFORMATION:
NAME: Warburg, Richard J.
                                NEORMATION FOR SEQ ID NO: 83:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
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SOFTWARE: WOR'D PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
DELGA ADDITION: 435
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                                                                                 REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                      ZIF: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
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                                                                 TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                    REGISTRATION NUMBER:
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90071-2066
                                                    (: (213) 955-0440
67-3510
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2185 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sun, Dongxu
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Lee, Ving J.
Malouin, Francois
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Pred. No. 1
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US-08-317-880-5
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; STRANDEDNESS: sing;
; TOPOLOGY: linear
US-09-265-315-83
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Best Local S
Matches 62
                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,880
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: BOSGIETY PORNAMINE:
                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1634
TELEPAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1549 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hall, Linda M.
TITLE OF INVENTION: Proteins for
TITLE OF INVENTION: and Function
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                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
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                                                                                                        553 cagaactcagacacaacctacagattatatgattatgaccgaaaagatgcagaaggcaag 612
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CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Rogalskyj, Peter REGISTRATION NUMBER: 3
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les 62; Conserv
                                                                                                                                                                                                                                                                              TOPOLOGY:
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CCAAGTCACTTCTAAACGAAATTGCGTATAGAATGCGTATAGAAGCATCCGCATCTGCAT 1288
                     14603
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                                                                                                                                                3.1%; Score 29.2; ilarity 48.8%; Pred. No. 11; Conservative 0; Mismatches
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Pred. No. 10;
                                                                                                                                                Mismatches
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                                                                                                                                                83;
                                                                                                                                                                                 Length 1549;
                                                                                                                                                Indels
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US-08-782-396-5
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NESULT 13
US-08-152-271-1
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Best Local Similarity
Matches 79; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/317,880
APPLICATION NUMBER: US 08/317,880
APILING DATE: 04-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: ROGALSKYJ, Peter
REGISTRATION NUMBER: 38,601
REFERENCE/DOCKET NUMBER: 19226/611
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1634
TELEPHONE: (716) 263-1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (716) 263-1600 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
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STREET: Cli...
CITY: Rochester
CTTATE: New York
TI S.A.
                                                                            1289 CAGCATCCGCATCCATCAATAAACTGCACTTTTGCGCATA 1330
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                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PROTEINS FOR CATION CHANNEL EXPRESSION TITLE OF INVENTION: AND FUNCTION NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hall, Linda M. APPLICANT: Feng, Guoping
                                                                                                       673 cggcatacagttcaccatgaacaaattgaggatttgcttaca 714
                                                                                                                                                                                                                                                                                    553 cagaactcagacacaacctacagattatatgattatgaccgaaaagatgcagaaggcaag 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM FC COMPUTER: IBM FC COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPTWARB: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1549 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                      cggcatacagttcaccatgaacaaattgaggatttgcttaca 714
                                                                                                                                                                CCAAGTCACTTCTAAACGAAATTGCGTATAGAATGCGTATAGAAGCATCCGCATCTGCAT 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14603
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                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JAN-1997
                                                                                                                                                                                                                                                                                                                                               3.1%; Score 29.2; DB 48.8%; Pred. No. 11;
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Sequence 1, Applicati Patent No. 5583039 GENERAL INFORMATION:

Application US/08152271

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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/534,679
FILING DATE: 07-JUN-1990
APPLICATION NUMBER: KOREAN NO. 5:
APPLICATION NUMBER: KOREAN NO. 5:
APPLICATION NUMBER: APPLICATION:
NAME: DUNN, MICHAEL L.
NAME: DUNN, MICHAEL L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: ATTORNEY; 716-433-
INFORMATION FOR SEQ ID NO: 1:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                       FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO
                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                         DESCRIPTION: The nucleotide sequence of 2471 bp DNA frag-
pescription: ment of B. licheniformis containing an open reading frame
DESCRIPTION: capable of encoding a maltogenic amylase, its 5' and 3'
DESCRIPTION: sequences, and 578 amino acid deduced sequence of the
DESCRIPTION: open reading frame.
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OPERATING SYSTEM: MS-DOS
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REGISTRATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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TOPOLOGY: cir
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                   IDENTIFICATION
                                                    LOCATION:
                                                                                                            NAME/KEY:
                                                                                                                                                                                  DEVELOPMENTAL STAGE:
                                                                                                                                                                                                     INDIVIDUAL
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                                    LOCATION:
                                                                         LOCATION:
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441-744
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Cha,
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Kim, Jeoung Ryel
Seo, Byung Cheol
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                                                                                                                                                                                                                                                                                                                                                                                                                                          circular
               B. licheniformis Maltogenic Amylase putative promoter; 197-202 (-35), 235-2 putative ribosome binding site; 282-287 putative translation initiation site; 2 translation termination site; 2026 TION METHOD: by similarity with known
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Department of Food Science and Technology,
College of Agriculture and Life,
Seoul National University
                                                                                                                                                                                                                                        Gram positive Bacterium
                                                                                                                                                                                                     ISOLATE:
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N: A Method for Isolating Gene of
Notation and to Produ
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or to an established consensus
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                       with known sequence
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US-08-317-880-1
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Best Local
                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Hall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION INFORMATION: AUTHORS: KIM, IN CHEOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1997
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2117
                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
         ATTORNEY/AGENT INFORMATION: NAME: Rogalskyj, Peter
                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               735 ttacttttcggtggggaaatggaacttatcaggatcagcaagcttaaagcagcaaaaacc 794
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OTHER INFORMATION:
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VOLUME:
                                                                                                                                                                                                              CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISSUE: NO. 31
PAGES: 22108-22114
DATE: 05-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS:
                                          FILING DATE: 0'CLASSIFICATION:
                                                                         APPLICATION NUMBER:
                                                                                                                                                                                  ZIP: 14603
                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                            ADDRESSEE:
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTCATTTTTGGGGCGGTCTAAATTCTGTTAGGCCTAACAGGTTTAAAACTATTGTAAGC 2056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTTCTGTCGAGGATTACAATTGTCTCAGATTCCAAGATAGAAGGGGGGAAAAAAGATGCA 2116
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACATTTAAAAAAAGGAATTTTAGTGCTGCTGGCGTCAGTTCT 2158
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79; Conserv
                                                                                                                                                                                                              Rochester
New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JANG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHOI, YANG DO PARK, KWAN HWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                           Nixon, Hargrave, Devans & Doyle inton Square, P.O. Box 1051
                                                          04-OCT-1994
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                                                                                                                                                                                                                                                                                                                                      Linda M.
                                                                                                                                                                                                                                                                                                       Proteins for Cation Channel Expression and Function
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              has transferase activity.
                                                                         US/08/317,880
38,601
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E. coli transformants harboring
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19226/610 (R-5261)

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COMPOUTER: IBM PC COMPACTIBLE
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PStentIn Release #1.0, Version #1.30
COURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/782,396
FILING DATE: 13-7M-1997
CLASSIFICATION UNMBER: US 08/317,880
FILING DATE: 04-OCT-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/317,880
FILING DATE: 04-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: ROGALSKy1, Peter
REGISTRATION NUMBER: 38,601
REFERENCE/DOCKET NUMBER: 19226/611 (R-5261B)
TELECHONE: (716) 263-1634
TELECHONE: (716) 263-1634
INCOMMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3954 base pairs
TYPE: DUCLES CATERISTICS:
LENGTH: 3954 base pairs
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US-08-782-396-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.1%;
Best Local Similarity 48.8%;
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08782396 Patent No. 5871940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (716) 263-1600 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hall, Linda M.
APPLICANT: Feng, Guoping
TITLE OF INVENTION: PROTEINS FOR CATION CHANNEL EXPRESSION
TITLE OF INVENTION: AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Ha
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
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STRANDEDNESS: single
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                     nucleic acid
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Pred. No. 20;
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US-08-782-396-1
          DNA (genomic)
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Best Local Similarity
3690 CAGCATCCGCATCCGCATCAATAAACTGCACTTTTGCGCATA 3731
                                                       3630 CCAAGTCACTTCTAAACGAAATTGCGTATAGAATGCGTATAGAAGCATCCGCATCTGCAT 3689
                                                                                                               553 cagaactcagacacctacagattatatgattatgaccgaaaagatgcagaaggcaag 612
                    673 cggcatacagttcaccatgaacaaattgaggatttgcttaca 714
                                                                             613 ctgcgcgagcttcatctgaaaaagagcattgaagtgatagaggtccccgtctattccagaa 672
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Pred. No. 20;
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Search completed: May 17, 2001, 15:33:22 Job time: 2467 sec

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em\_esthum24:\*
em\_esthum25:\*

em\_esthum21:\*
em\_esthum22:\*

em\_esthum26:\*
em\_esthum27:\*
em\_esthum28:\*
em\_estin1:\*
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em\_esthum14 \*
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em\_esthum18 \*
em\_esthum19 \*
em\_esthum20 \*

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em\_esthum11:\*
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Maximum DB
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Perfect score:
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Listing first 45 summaries
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 May 17, 2001, 11:56:34; Search time 1125.86 Seconds (without alignments) 7332.717 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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em\_estro18:\*

em\_estro19:\*
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em\_estro9

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Result
No.
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   341.2
39.8
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38.2
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Match
    em_gss_pln1:
em_gss_pln2:
em_gss_rod1:
em_gss_rod3:
em_gss_rod4:
em_gss_rod4:
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em_gss_rod5:
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966
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   CNS005TE
CNS016E2
AQ07084A
CNS05PX4
AQ675159
AA6575159
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AA675159
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BBF15061
BF15061
BF72777
BB200184
CNS00196
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ACNS00196
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BB200489
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AL1060767 Drosophil
AL1106628 Drosophil
AQ1106644 HS\_2256\_A
AL248529 Tetracdon
AQ675159 HS\_2162\_A
AA550191 1307m3 gm
BF628576 HVSmEb000
AQ137339 HS\_3058\_B
BF815061 MR2-CI012
AZ209683 SP\_0138\_A
AZ0942470 CpG1126A
AL197004 Tetracdon
BF727776 1000052F0
AL072060 Drosophil
AL1063921 Drosophil
AL1063921 Drosophil
AL1075573 Drosophil
AL075573 Drosophil
BB200489 BB200489

Description

9b\_est48:
9b\_est50;
9b\_est50;
9b\_est50;
9b\_est50;
9b\_est53;
9b\_est53;
9b\_est53;
9b\_est56;
9b\_est60;
9b\_est60;
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RESULT 1
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VERSION |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                   source
                                                                                                            Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Maron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NV. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library, or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fly), genomic survey so
AL060767
AL060767.1 GI:4943573
                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 997)
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR12K22 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                 Direct
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                                                                                found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fruit fly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic survey sequence.
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                                /organism="Drosophila
/db_xref="taxon:7227"
              /clone_lib="RPCI-98"
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1 AQ075795
5 BF320729
AI408821
0 BE861867
4 AQ992818
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CNS011PE
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                                                melanogaster'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL104242 Drosophil
AA111946 zn53e09.r
AL447600 Parameciu
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AQ992818 RPCI-23-2
BF113227 EST440817
AQ692130 HS_5328_B
BE460767 EST412186
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AW463593 BP230013A
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BF320729 uz55907.y
AI408821 EST237112
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AL100556 Drosophi
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AL288205
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AQ586301 RPCI-11-4
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CNS016E2/c
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KEYWORDS
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                                                                                                                              Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                        fly), ger
AL106628
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                                                                                                                                                                                                                                                                    Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS.
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                              /organism="Drosophila melanogaster"
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                                                                                                                                  Plate: 2256 rov
Class: BAC ends
                                                                                                                                                                            401 Queen Anne Avenue North, Sea
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                   University of Washington
                                                                                                                                                                                                                                                                                                  scanning the human genome Proc. Natl. Acad. Sci. U.
                                                                                                                                                                                                                                                                                                                                                Hood
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HS_2256_A1_H03_MF CIT Approved Human Genomic
saplens genomic clone Plate=2256 Col=5 Row=0,
AQ070844
                                                                                                                                                               Sequence Tagged Connector
                                                                                                                                                                                                                                                                     Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                       99380589
                                                                                                                                                                                                                                                                                                                            Sequence-tagged connectors: A sequence approach to mapping
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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172 c
                                                                        /organism="Homo sapiens"
'note="Organ: sperm; Vector: pBeloBAC11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCTATTATGGCATCTAGAGGTTAAGCAGCTTGCCAGGTTCAATAAGTCAAGCAGTGGGA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agctcttgcgccgtgtaaaggtaaagccgggggattttttctatgtgccaagcggtactg 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACACACCAGGTGTTTCTAAACAGAAGCAGAGTAGAGACACAGACACCTAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGAGGATAAAGCTATAGGTTTCCTTGTCTTCCAGATGGTAGCAGAGTGAGATAAGACCT
                                                                                                                                                                                                                                   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a lar scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 1095)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetler, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                   Human gene number estimate provided Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleosto; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleos Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Holacanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNS05PX4 1095 bp DNA GSS 26-MAY-2000 Tetraodon nigroviridis genome survey sequence SP6 end of clone 010B15 of library B from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                 Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weissenbach, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roest-Crollius, H., Jaillo
Bouneau, L., Billault, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS; genome survey sequence. Tetraodon nigroviridis.
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                                                                                                                                                                                                                                                                                                                                  Submission
                                                                                       /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="010815"
/clone_11b="B"
/clone_11b="B"
/note="Genoscope sequence ID : COA
258 c 204 g 292 t 35
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                                                                                                                                                                                                                     Location/Qualifiers
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51.8%;
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Euteleostei; Neoteleostei;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTGCAGTGAGAGAAGGCGCCTGCCTTCCACGGACTGCCAAAGGGTTAGGCAGAGCAGCA 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acgacattgattgaatgcgcttacttttcggtgggaaatggaacttatcaggatcagca 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTTGTTGTGTCTGTTTACTTTTTTTTTTTAAAAAGCTGTTAGTCTGT
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                                    tcccgtctattccagaacggcatacagttcaccatgaacaaattgaggatttgcttacaa 715
                                                                                                       aagatgcagaaggcaagctgcgcgagcttcatctgaaaaagagcattgaagtgatagagg 655
               TTCTATCAGGACAAACACCACAAAGTGTATGGATACAATGAATTCAAGAGCCACACTCAT
                                                                             AAAAGGGAGACAAATAGTCTAAAGGCCTTTATCGTAAAGAATAAAATGTCTAGTTTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ675159 419 bp DNA GSS
HS_2162_A1_G09_T7C CIT Approved Human Genomic :
sapiens genomic clone Plate=2162 Col=17 Row=M,
AQ675159
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1 (bases 1 to 419)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                             Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2162 row: M column: 17
Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 419.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scanning the human genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                110
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natl. Acad. Sci. U. S. A.
                                                                                                                                                                                                                                              /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones E-Coli DH10B" a 99 c 77 g 133 t
                                                                                                                                                                                                                                                                                                             /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="platce=2162 Col=17 Row-M"
/clone_1ib="CIT Approved Human G
                                                                                                                                                                                                                                                                                             /sex="male"
                                                                                                                                                             46.38;
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                                                                                                                                            Score 38.4; DE Pred. No. 1.8; 0; Mismatches
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Sperm Library D
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AUTHORS
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               317
                                                  389
TAAATATACATTATGTTTTCTCTTATAAACAAAATTCAGATGCAACAAGTTTTTACGTGC 330
                                                                    tagatgötgaccaggacttatotgttcaggtgcatcogaatgatgaatatgccaacatac 316
                                                                                                                   97;
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멍 Qy 밁 Ş

Similarity 49.9 37; Conservative

0

Mismatches

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Gaps

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Score 38.2; Di Pred. No. 2.1;

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Fax: 352 392 9704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dame, J.B., Arnot, D.E., Bourke, P., Chakrabarti, D., Christodoulou, Z.,, Coppel, R., Cowman, A., Craig, A., Fischer, K., Foster, J., Goodman, N., Hinterberg, K., Holder, A.A., Holt, D., Kemp, D., Lanzer, M., Lim, A., Newbold, C., Ravetch, J.V., Reddy, G.R., Rubio, J., Schuster, S.M., Su, X.-Z., Thompson, J.K., Vital, F., Wellems, T.E. and Werner, E. Current status of the Plasmodium falciparum genome project Mol. Biochem. Parasitol. 79, 1-12 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone 1307m, DNA sequence.
AA550191
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1307m3 gmbPfHB3.1, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: damej@mail.vetmed.ufl.edu
Seq primer: T3
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                                                                                                                                       /note="Vector: pBlueScript SK(+); Genomic DNA, from asynchronous blood stage parasites of the cloned Honduran HB3 isolate cultured in vitro, was digested with mung bean nuclease in the presence of 30% formamide at 50cC (Vernick K.D., Imberski, R.B., and McCutchan, T.F. 1988. Nucleic Acids Research 16:6883-6896). The ends of the fragments
                        were polished using T4 DNA polymerase, and the fragments were ligated to EcoR V-cleaved and dephosphorylated pBlueScript SK(+). Recombinant plasmids transformed E. coli XL1-Blue."
                                                                                                                                                                                                                                                                                                                   /clone="1307m"
/clone_lib="gmbPfHB3.1, G. R
/lab_host="E. coli XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Plasmodium falciparum"
/db_xref="taxon:5833"
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RESULT
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                                                                      AAGAATCACTGCTAAGGCAACAGGAGCAGCAGAAACTAGCTGAAGAGTTCCTACTGAGGC
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AGCAAGATCAGCAAAGGCTAGCTGAAGAACAATCCCGTACTACTTCTCTGGAGGTTGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 Jordan Hall, Člemson, SC 296:
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clemson University
Clemson Hall, Clemson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wing RA
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Development of a genetically and physically anchored EST resource for barley genomics unpublished (2000)
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
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Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo
Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
                                                                                                                                                                                                                                                                                                                                                                /Clone-"HYSMED0005J18f"
/Clone_lib-"Hordeum vulgare seedling
HVcDNA0002 (Dehydration stress)"
/tissue_type-"Seedling shoot"
/lab.host="TJC121"
                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Hordeum vulgare"
/cultivar="Morex"
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                                                                        ATCTGAAGTAGTGCTTATGAAGAGCTTGTTGAAACGATAGAAGATCTTCATGATATTATG
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HS_3058_B1_E03_MR CIT Approved Human Genomic:
sapiens genomic clone Plate=3058 Col=5 Row=J,
AQ137339
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Plate: 3058 row: J colu
Class: BAC ends
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401 Queen Anne Avenue North, Seatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 375)
Mahairas,G.G., Wallace,J.C., Smith,K:, Swartzell,S., Holzman,T.,
Mahairas,G.G., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. al
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Location/Qualifiers
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Fax: (206) 616-3887
Email: jwallace@u.washington.edu
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                                                                                                                                                                                                                                                                                                                                  /note="Organ: sperm; Vector: pBeloBAC11; BAC E-Coli DH10B" 71\ c 67\ g 115\ t 1 others
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/clone="Plate=3058 Col=5
/clone_lib="CIT Approved
                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
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                                                                                                                                                           GAAAGAACTTCAAACTATGAAGGCGGACTTAACCCGGCACGTTCTCGTGGAAGATGTGAT 314
                                                                                                                                                                                 ggaagaactaactaccatgatagagcgtggagaatgggatgaagctcttgcgccgtgtaaa 470
aattottgotttggagacgcagcagaactcagaccaacctacagattatatgattatga
                                                                                                            ggtaaagccgggggattttttctatgtgccaagcggtactgttcatgcgattggaaaagg
                                                                    GGTTTTGAAGGAGCAAATAGAGCATTTGC--ACAGACAATGGGAGGACCTCTGCTTAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dias Neto,E., Garcia Correa,R., Verjovski-Almelda,S., Ellumes, M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Ragai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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MR2-CI0128-011200-004-b09 CI0128 Homo sapiens cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2-CI0128-
011200-004-b09&t3=2000-12-01&t4=1)
Seq.primer: puc 18 forward
Seq.primer: puc 18 forward
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence tags
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                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                           /note-"Organ: colon_ins; Vector: pucl8; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application NO. 196.716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="Adult"
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/clone_lib="CI0128"
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                             ttgcttacaacgacattgattgaatgcgcttacttttcggtggggaaatggaacttatca 765
TTGGACACAACGAAATTGCATTATCACTGATTAATTATGCTGTTGATTTTGGATTTACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                      91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: acameron@caltech.edu
plate: 138 row: A column:
Seq primer: T7
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1 (bases 1 to 889)
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Fax: (626) 793-3047
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Pasadena California 91125, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                      /note="Organ: Sperm; Vector: BACe3.6; BAC Clones in E-Coli DH10B"
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/clone_lib="Strongylocentrotus purpuratus, purple
urchin, sperm genomic BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
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                                                                                               AGATTTGGTAGTTATTTTGGATTTGTAAAGAATAAAATGAGAAAA 561
                                                                                                                                                     agatgccgagattatttatggccacaatgcaacaacaaaggaaga 416
                                                                                                                                                                                                                                                                                                                                                    AATATTGGAAATTTAATTGGATGTAACTTTTATTTTACTATAAAAAAATCAAGGTATCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For Annotation Data see http://medsfgh.ucsf.edu/id/CpTags/home.html Seq primer: M13(-21) forward
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Tel: 415 206 8846
Fax: 415 206 3353
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1 (bases 1 to 799)
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//clone_lib="CploWagDNA1"
//lab_host="E. coli XL2 Blue MRF'"
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library were selected for sequence analysis using T3 and
//lab_host="E. coli Station XL2 Blue
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/strain="IOWA"
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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/db_xref="taxon:99883"
/clone="138N19"
/clone_lib="G"
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Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR33M19 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: walbot@stanford.edu
Plate: 1000052 row: F co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
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                 karyota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
erygota; Neoptera; Endopterygota; Diptera; Brachycera;
scomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="dbEST:707007G07.x2"
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RESULT 15
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            750 ATGMTKCKKWAWTKTAWAMRARMTAMAWDATRTAMAAATWDTDWATAKTTMCTRMSMMMC 809
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
             Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <a href="http://www.fruitily.org">http://www.fruitily.org</a> The BDGP Drosophila melanogaster BAC 11 threat the Drosophila melanogaster BACS.
                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                          Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                 Genoscope.
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melanogaster BAC library was prepared by Kazutoyo Osoegawa and
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/note="end : T7"
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BASE COUNT
ORIGIN
Search completed: May 17, 2001, 15:08:04 Job time: 11490 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1029 WDKWWWWATAAKTDTAWTWWRTAWRADWAGRDRGAGKRDRDAATDADGAGRRDGGRKRKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             762 atcaggatcagcaagcttaaagcagcaaaaaccattccttcttatcagtgtgattgaagg 821
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-Q-/cgn2_1/USPTQ_spool/US09462846/runat_17052001_115429_970/app_query.fasta_1.376
-DB-N_Geneseq_0401 -QFMT-fastap -SUFFIX-p2n.rng -GAPOP=12.000
-GAPEXT=4.000 -MINANTCH-0.100 -LOOPL-0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP-10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500
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-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
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-WAIT -THREADS=1
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to cleave fusion proteins
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This sequence represents the Bacillus subtilis cysteine protease CP1 coding sequence. The invention relates to new Gram-positive bacteria, especially Bacillus, containing mutations in, or deletion of, at least part of the gene encoding cysteine protease (CP)1, CP2 (x25734) or CP3 (X25735), so that CP-related proteolytic activity is lost. The bacteriare used for expressing heterologous proteins, particularly hormones, growth factors, cytokines or especially enzymes, e.g. protease, carbohydrase, lipase, isomerases (racemase, epimerase, tautomerase or mutase), transferase, kinase and phosphatase. CP1-3 are used e.g. in soaps, dishwashing compositions, contact lens cleaners or laundry detergents, also for peptide hydrolysis, waste or textile treatment, the colored contact the contact of the contact of the colored contact the contact of the contact of the colored contact of the colored contact of the colored colored contact of the colored colored colored contact of the colored col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gram-positive bacterium with mutated or deleted gene protease 1, 2 or 3 - used to express proteins with re
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              GluPheLysLeuGluGlyTyrAlaGluCysIleValSerHisLeu 315
                                                  GAATTTAAACTCGAAGGATATGCAGAATGTATCGTCTCCCATCTG
                                                                                                          TCTTATCAGTGTGATTGAAGGGGGGGCCGTATGATCTCTGGTGAGTATG
                                                                                                                         uLeuIleSerValIleGluGlyGluGlyArgMetIleSerGlyGluTyrV 284
                                                                                                                                                             LysTrpAsnLeuSerGlySerAlaSerLeuLysGlnGlnLysProPheLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluLeuLeuArgArgValLysValLysProGlyAspPhePheTyrValPr 167
                                                                                                                                                                                                                    AGGATTTGCTTACAACGACATTGATTGAATGCGCTTACTTTTCGGTGGGG
                                                                                                                                                                                                                                  luAspLeuLeuThrThrThrLeuIleGluCysAlaTyrPheSerValGly
                                                                                                                                                                                                                                                                                        eGluValProSerIleProGluArgHisThrValHisHisGluGlnIleG
                                                                                                                                                                                                                                                                                                                               GCAGAAGGCAAGCTGCGCGAGCTTCATCTGAAAAAGAGCATTGAAGTGAT
                                                                                                                                                                                                                                                                                                                                                                                    AGCAGAACTCAGACAACCTACAGATTATATGATTATGACCGAAAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCGGTACTGTTCATGCGATTGGAAAAGGAATTCTTGCTTTGGAGACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGlyGlyThrAlaLeuAlaAspPheGlyTyrThrIleProSerGlnArgT 34
                                                                                                                                                                                                                                                                          AGAGGTCCCGTCTATTCCAGAACGGCATACAGTTCACCATGAACAAATTG
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seq_documentation_block:
ID X25735 standard; DNA;
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AC X25735;
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Cysteine protease; Gr
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Bacillus subtilis.
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                                                                            This sequence represents the Bacillus subtilis cysteine protease CP3 coding sequence. The invention relates to new Gram-positive bacteria, especially Bacillus, containing mutations in, or deletion of, at least part of the gene encoding cysteine protease (CP)1 (X25733), CP2 (X25734) or CP3, so that CP-related proteolytic activity is lost. The bacteria are used for expressing heterologous proteins, particularly hormones, growth factors, cytokines or especially enzymes, e.g. protease or mutase), transferase, isomerases (racemase, epimerase, tautomerase or mutase), transferase, kinase and phosphatase. CP1-3 are used e.g. in soaps, dishwashing compositions, contact lens cleaners or laundry detergents, also for peptide hydrolysis, waste or textile treatment, to cleave fusion proteins and as animal feed additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gram-positive bacterium with mutated or deleted gene for cysteine protease 1, 2 or 3 - used to express proteins with reduced proteolytic degradation, e.g. proteins, growth factors or enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 6A-B; 31pp; English.
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P-PSDB; W99373.
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alignment_block:
US-09-462-846-2 x X25735
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GGGCGGAACCGCTTTACGAGATAGATTTGGATACAGTATTCCTTCAGAAT
             pGlyGlyThrAlaLeuAlaAsp...PheGlyTyTThrIleProSerGlnA
                                                            MetThrThrGluProLeuPhePheLysProValPheLysGluArgIleTr
                                                ATGACGCAATCACCGATTTTTCTAACGCCTGTGTTTAAAGAAAAATCTG
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rgThrGlyGluCysTrpAlaPheAlaAlaHisGlnAsnGlyGlnSerVal

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                                       _documentation_block: x25734 standard; DN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGTACATTATCGACTGTAAGGAAAACGCAGAAATCATTTACGGGCATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspAlaGluGlyLysLeuArgGluLeuHisLeuLysLysSerIleGluVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspGluTyrAlaAsnIleHisGluAsnGlyGluLeuGlyLysThrGluCy 116
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                                                                                                                                                           GlyGluPheLysLeuGluGlyTyrAlaGluCysIleValSerHisLeu 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lIleGluValProSerIleProGluArgHisThrValHisHisGluGlnI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATAGCAACGGAAGTCCGAGAGAGCTTCATTTTGCCAAAGCGGTCAATGC
                                                                                                                                                                                                                                                                                                  TCTGATTTGCAGCGTGATAGAAGGAAGCGGTTTGCTCAAGTATGAGGACA 850
                                                                                                                                                                                                                                                                                                                                     eLeuLeuIleSerValIleGluGlyGluGlyArgMetIleSerGlyGluT
                                                                                                                                                                                                                                                                                                                                                                                TATAAATGGGACATCAATGGCGAAGCTGAAATGGCTCAGGATGAATCCTT
                                                                                                                                                                                                                                                                                                                                                                                                               GlyLysTrpAsnLeuSerGlySerAlaSerLeuLysGlnGlnLysProPh 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCCACGGTTCCCCATGTGGACGGGTATATAGATGAATCGACAGAATCAA 700
                                                                                                                                        CCCGATTTTACGATAAAAGGAACTTGTACCCTTATCGTGTCTCATATT 948
                                                                                               /SIDS6/gcgdata/geneseq/geneseqn/NA1999.DAT:X25734
                                       DNA; 945
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alignment_block:
US-09-462-846-2 x X25734
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                                                                                                                                                                                                                                   Align seg 1/1
                                                                                                                                                                                                                                                                                                           Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                           coding sequence. The invention relates to new Gram-positive bacteria, especially Bacillus, containing mutations in, or deletion of, at least part of the gene encoding cysteine protease (CP)1 (X25733), CP2 or CP3 (X25735), so that CP-related proteolytic activity is lost. The bacteria are used for expressing heterologous proteins, particularly hormones, growth factors, cytokines or especially enzymes, e.g. protease, carbohydrase, lipase, isomerases (racemase, epimerase, tautomerase or mutase), transferase, kinase and phosphatase. CP1-3 are used e.g. in soaps, dishwashing compositions, contact lens cleaners or laundry detergents, also for peptide hydrolysis, waste or textile treatment, to cleave fusion proteins and as animal feed additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gram-positive bacterium with mutated or deleted gene for cysteine protease 1, 2 or 3 - used to express proteins with reduced proteolytic degradation, e.g. proteins, growth factors or enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cysteine protease; Gram-positive bacteria; mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B.subtilis cysteine protease CP2
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the Bacillus subtilis cysteine protease CP2
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P-PSDB; W99372.
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                                                        104
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                                                                                                                                                                            ThrGluProLeuPhePheLysProValPheLysGluArgIleTrpGlyGl
                        AsnGlyMetTyrLysGlyPheThrLeuSerGluLeuTrpGluHisHisAr
                                                                         lyGluCysTrpAlaPheAlaAlaHisGlnAsnGlyGlnSerValValGln
                                                                                                                   GACGAAGCTTCGTGACGCTTTTGGCTACGCAATACCCTCACAAAAAAACAG
                                                                                                                                  yThrAlaLeuAlaAsp...PheGlyTyrThrIleProSerGlnArgThrG
                                                        GTGAGTGCTGGGCCGTTTCTGCACATGCCCATGGCTCGTCGTCTGTAAAA
AATGGCCCGCTGGCAGGAAAGACACTTGATCAAGTATGGAAAGATCATCC
                                                                                                                                                                                                                                                                                                                                          Quality:
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3.804
80.511
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seq_documentation_block:
ID X13110 standard; DNA,
XX
AC X13110;
XX
DT 19-MAR-1999 (first &
XX
DT 19-MAR-1999 (first &
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KW Enterococcus faecalis
XX
KW Enterococcus faecalis
                                                                                                                                                                                                 seq_name:
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                                                                                                                                           X13110 standard; DNA; 12438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGCTGAGATCATTGTTTATGTGCAATCAGATTATTTCTCAGTGTACAAA
                                                                                                                                                                                                                                 TTTACAATAGAAGGAACATGTGAATTCATGATATCTCAT
                                                                                                                                                                                                                                                                PheLysLeuGluGlyTyrAlaGluCysIleValSerHis 314
                                                                                                                                                                                                                                                                                                     ATGAATGCAATGCAGGCTCACACTTTATTCTGCCTGCGCATTTTGGAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leLeuAspAlaAspGlnAspLeuSerValGlnValHisProAsnAspGlu 101
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TGCTGGACGCCAATATGGATCTCTCCGTGCAAGTCCATCCTGATGATGAT 303
                                                                                                                                                                                                                                                                                                                                                                          GGGGAGTGTTCTGAGCGGATCAGGACGAATCATAAATAATGGTATTCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAACTCTGATACAACATATCGCGTATACGATTATGACCGCTGTAATGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuLeuArgArgValLysValLysProGlyAspPhePheTyrValProSe 168
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                                                                                                                                                                                             /SIDS6/gcgdata/geneseq/geneseqn/NA1999.DAT:X13110
faecalis; contig; detection;
                                 faecalis genome contig SEQ ID NO:173.
                                                                      (first entry)
                                                                                                                                             ВP
Enterococcal infection;
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alignment_scores:
Quality:
Ratio:
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US-09-462-846-2 x X13110
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                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                        6426
                                                                                                                       6376
                                                                                                                                                                                                                                                      6276 GAACCATTATTTTTACAACCTGTTTTTCAAGAAAAATTTTGGGGCGGCAA 6325
                                                                                                                                                                                      6326 TCGTCTACACACGCTATTTGGTTTCGATTTACCGAGCGATAAAATTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 963-969; 2084pp; English.
                      69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12438
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                                                                                                                                                                                                                                                                         4 GluProLeuPhePheLysProValPheLysGluArgIleTrpGlyGlyTh
rAlaLeuAlaAsp...PheGlyTyrThrIleProSerGlnArgThrGlyG
                                                   GGCGAATTTAAAGGAAAAAATTAGATGAATTGTGGGCAGACCATCAAGA
                                                                        GlyMetTyrLysGlyPheThrLeuSerGluLeuTrpGluHisHisArgHi 69
                                                                                                                     AAGATTGGGCAATCAGTGCACATCCACATGGCGTTAGTACTGTTTTAAAT
                                                                                                                                     luCysTrpAlaPheAlaAlaHisGlnAsnGlyGlnSerValValGlnAsn
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97US-0044031.
97US-0046655.
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3.553
77.603
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Percent Identity:
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53.628
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seq_name: /SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:V52181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyLysLeuArgGluLeuHisLeüLysLysSerIleGluValIleGluVa 219
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                                                                                                                                                                                                                                                                                                                                                                     ACAGATATTCCGAGCTGGCGTTTTGAAGGTGATCTAACGATTATAGCTTC
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                       pneumoniae genome fragment SEQ
                            IJ
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alignment\_block: US-09-462-846-2 x V52181/rev

Percent Similarity:

Align seg 1/1 to reverse of: V52181

from: 1 to: 25002

2331 AGCCAAGCTACGTGATGAGTTTGGCTACGACATCCCAAGTGAAAAAATCG

lyGluCysTrpAlaPheAlaAlaHisGlnAsnGlyGlnSerValValGln 51

yThrAlaLeuAlaAsp...PheGlyTyrThrIleProSerGlnArgThrG

2332 35

19

2381 TCAGAACCATTATTTTACAATCAGTTATGCAAGAAAAATCTGGGGTGG

3 ThrGluProLeuPhePheLysProValPheLysGluArgIleTrpGlyGl

alignment\_scores:

Quality: Ratio:

841.00 3.461 76.899

Percent Identity:

Length: Gaps:

316 5 53.797

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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (V55134 to V55524) recorded con it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (V52134 to V55524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S. pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a compose of the sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hypridise to the target sequence and isolating the nucleic acid color molecules from the members; or (b) isolating mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the sequence and isolating the amplification and colorating the amplified sequences. The computer readable medium can be used in a computer based system for identifying fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds.
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Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
                                                                                      S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 431-445; 1409pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-272225/24.
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Sequence 25002 BP; 7422 A; 5498 C; 4618 G; 7463 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                            compositions and vaccines
                                                                 invention can be used in diagnosis kits and assays, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choi GH,
Rosen CA;
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                                            for S. pneumoniae.
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                                                                 pharmaceutical
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16-MAR-1999

(first entry)

ВP

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access

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seq_name:
                                                                                                                                                                                                                                                                             1643
                                        1493 GAAGCTTGGAACTCTGGAAGGCAAGGTTTGGAATTGATTAGCCAT
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                                                                                                                                                                                                                                                                         TACAAGTGGGAAATTACTGGAAAAGTTGACTTTGAAAAGACAGCTGACTA 1594
                                                              GlyGluPheLysLeuGluGlyTyrAla...GluCysIleValSerHis
                                                                                                                                           yrValTyrProPheLysLysGlyAspHisMetLeuLeuProTyrGlyLeu 299
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                                                                                                                                                                                              CAGCTTATTGAGTGTCTTGGCTGGTCAAGGTCAGCTAACTGTTGACGGGA 1544
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                                                                                                                                                                                                                                                                                                                                                                                                                               CATTGGTGAGCCAGCAATAGCCGTCCTGTAACTGTT
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Claim
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                                                                                            Polynucleotide(s) and
                                                                                                                     WPI; 1997-374922/35
                                                                                                                                              Rosen
                                                                                                                                                         Barash SC,
                                                                                                                                                                                                                              07-JAN-1997;
                                                                                                                                                                                                                                                       30-JUL-1997.
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                                                                                                                                                                                 ( HUMA - )
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                                                                                                                                              CA;
                                                                      .aureus
                                                                                on
                                             Page 816-822;
                                                                               otide(s) and proteins derived computer readable medium and
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                                                                      vaccines
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/note=
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                                                                                                                                                         Dillon
                                                                                                                                                                                                                                                                                                                                                                                                   = "these bases :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering are included to maintain the received by the DNA sequence."
                                           3271pp;
                                                                                                                                                                                                                                                                                                             "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
                                                                                                                                                                                                                                                                                                                                                                                                                                              "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "these
                                                                                                                                                                                                                                                                                                                                                                       'these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
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equence listing in the specification. For
noluded to maintain the nucleotide numberly
in the specification for this DNA sequence"
                                           English.
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                                                                                                                                                         Fannon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification
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                                                                                                                                                         MR,
                                                                               Staphylococcus aureus in the production of
                                                                                                                                                         Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for this
                                                                                                                                                         CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA sequence
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Sequence 9623 BP; 3025 A; computer readable medium.

1508 C; 1655 G;

3072 T;

363 other;

for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the

memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelld infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                             euAspAlaAspGlnAspLeuSerValGlnValHisProAsnAspGluTyr 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      luCysTrpAlaPheAlaAlaHisGlnAsnGlyGlnSerValValGlnAsn
                yThrValHisAlaIleGlyLysGlyIleLeuAlaLeuGluThrGlnGlnA 186
                                                                                                           LeuArgArgValLysValLysProGlyAspPhePheTyrValProSerGl
                                                                                                                                                                                                                                                                                                                                              AlaAsnIleHisGluAsnGlyGluLeuGlyLysThrGluCysTrpTyrIl 119
                                                                                                                                                                                                                                                                                                                                                                                         TAGATGCCAATGATAAATTATCTGTTCAAGTTCACCCAGATGATGACTAC
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CACTGTCCATGCCATTGGTTCGGGTATTTTAATTTTAGAGACACAACAAT
                                                                                                                                                      ATAAACAGACGTTAATAGACATGATTGATAATCATGAATTTGACAGTCTT
                                                                                                                                                                                      hrLysGluGluLeuThrThrMetIleGluArgGlyGluTrpAspGluLeu 152
                                                                                                                                                                                                                                   NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGCGTACATGCACATA
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Ratio:
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The present sequence encodes a novel polypeptide, which is optionally expressed in NCIMB 40771. The polypeptide, and polynucleotide encoding it, are derived from Staphylococcus aureus. Cells expressing ligands binding the polypeptide can be used to isolated candidate compounds

that bind and inhibit the activity of the polypeptide.

compounds

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seq_documentation_block:
ID T80389 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus WCUH 29; antagonist; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus Gene #1 encoding cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-APR-1998
                                                                                                             New Staphylococcus aureus polynucleotide and polypeptide(s) - isolating antagonist of the polypeptide(s) useful as anti-bact
                                                                                                                                                         P-PSDB; W24296.
                                                                                                                                                                     WPI; 1997-435166/40
                                                                                                                                                                                                                                                           26-FEB-1996;
                                                                                                                                                                                                                                                                                     25-FEB-1997;
                                                                                                                                                                                                                                                                                                                28-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS6/gcgdata/geneseq/geneseqn/NA1997.DAT:T80389
                                                                                   4; Page 26-27; 117pp;
                                                                                                                                                                                                  MKR,
                                                                                                                                                                                                                              SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                  Hodgson
                                                                                                                                                                                                                                                           96GB-0004045.
                                                                                                                                                                                                                                                                                       97WO-GB00524.
                                                                                                                                                                                                                                                                                                                                                                                                    protection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2111 BP
                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                       isolation;
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                                                                                                                anti-bacterials
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                                                                                                                                                                                                                                                                                                                                                                                                                      immunogen;
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can be used as anti-bacterial compounds. The polypeptide may also be used as an immunogen to vaccinate an animal for protection against Staphylococcus aureus caused disease.

seq\_name: /SIDS6/gcgdata/geneseq/geneseqn/NA1997.DAT:V74326

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alignment_block:
US-09-462-846-2 x T80389/rev
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                         219
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                         Val
                                                              luGlyLysLeuArgGluLeuHisLeuLysLysSerIleGluValIleGlu 218
                                                                                                                                                                                                                                                                                                                                                                    sLeuPheGlyGlnLeuGluGlyAspArgPheProLeuLeuThrLysIleL
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| ||||||
                                                  ATGGTCAATTGCGTGATTTGCACTTAGAGCAAAGTAAAGATGTGATTGAA
                                                                                                                      nAsnSerAspThrThrTyrArgLeuTyrAspTyrAspArgLysAspAlaG 202
                                                                                                                                                        GGCACTGTCCATGCCATTGGTTCGGGTATTTTAATTTTAGAGACACAACA
                                                                                                                                                                         GlyThrValHisAlaIleGlyLysGlyIleLeuAlaLeuGluThrGlnGI 185
                                                                                                                                                                                                                          euLeuArgArgValLysValLysProGlyAspPhePheTyrValProSer 168
                                                                                                                                                                                                                                                                                       rThrLysGluGluLeuThrThrMetIleGluArgGlyGluTrpAspGluL
                                                                                                                                                                                                                                                                                                                                     eIle.AspCysGlnLysAspAlaGluIleIle.TyrGlyHisAsnAlaTh 135
                                                                                                                                                                                                                                                                                                                                                                                                                          TAGATGCCAATGATAAATTATCTGTTCAAGTTCATCCAGATGATGACTAC
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                                                                                                    ATCATCCGATACGACATACCGTATTTATGACTATGATAGACGAGATCCAN
                                                                                                                                                                                                            TTTTCAAACGTATACCTGTTAAGCCCGGTGACTTTTATTATGTTCCTGCT
                                                                                                                                                                                                                                                                TAATAAACAGGCGTTAATCGACATGATTGATAATCATGAATTTGGCAGTC
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences confit the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the Saureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against 5 aureus infection of Saureus in a sample. Saureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating computer readable medium.
                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide(s) and proteins derived stored on computer readable medium and anti-S.aureus vaccines
                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 255-257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer readable medium; vaccine;
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/note= These bases represent a line of missing text in
/note the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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"these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering the forthis DNA sequence."
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                                                                                                                                                                                                                                                                                                                                        3271pp; English.
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food poisoning; osteomyelitis; therapy;
d infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ided to maintain the nucleotide numbering
the specification for this DNA sequence
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510 G;

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other;

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alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                    AsnSerAspThrThrTyrArgLeuTyrAspTyrAspArgLysAspAlaGl 202
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eSerValGlyLysTrpAsnLeuSerGlySerAlaSerLeuLysGlnGlnL
                                    GAAATTATTGAAAACCATAAGTGTACACACATTGTATCGAATGATTTCTT
                                                                  GluGlnIleGluAspLeuLeuThrThrThrLeuIleGluCysAlaTyrPh 247
                                                                                                                                     .....ValProSerIle...ProGluArgHisThrValHisHis 230
                                                                                                                                                                        ATATAATGATAGACCGTTAAATATTGAAAAAGCTTTAGACGTTATTCAGT
                                                                                                                                                                                                                                             NNGTCAGACATTACATATAGACTTTATGATTCAATCGTCAAGATAATCA
                                                                                                                                                                                                                                                                                                                                              lyThrValHisAlaIleGlyLysGlyIleLeuAlaLeuGluThrGlnGln
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alignment_block:
US-09-462-846-2 x X20249/rev
                                                                   alignment_scores:
    Quality:
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                                          Percent Similarity:
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
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                                                                                                                                                                X20248 to X20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borrelia burgdorferi; spirochete; bacterium; pathogen; I epidemic relapsing fever; endemic relapsing fever; Lyme infection; diagnosis; characterisation; detection; ds.
                                                                                                                                                                                                                                                                                                                                         New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention
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                                                                                                                          Sequence 116277
                                                                                                                                                      Lyme disease
                                                                                                                                                                                                                                                                                              Claim 1; Page 672-737; 1128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              Clayton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrelia burgdorferi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281 GlyGluTyrValTyrProPheLysLysGlyAspHisMetLeuLeu 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy of infections, particularly Lyme disease
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                                                         Ratio:
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97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                                       rTyrArg.....LeuTyrAspTyrAspArgLysAsp.....
                                                                                                                                                     TATCTTAAGGGAGAT...TGCATTGAGCTTATGACCAATTCCGACAATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rGluLeuTrpGluHisHisArgHisLeuPheGlyGlnLeuGluGlyAspA 78
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                                                                                                                                                                                            IleGlyLysGlyIleLeuAlaLeuGluThrGlnGlnAsnSerAspThrTh 190
                                                                                                                                                                                                                                                                              ysValLysProGlyAspPhePheTyrValProSerGlyThrValHisAla 173
                                                                                                                                                                                                                                        ..........GluLeuThrThrMetIleGlu..........
                                                                                                                                                                                                                                                                                                                                                             .....LeuArgArgValL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....TyrGlyHisAsnAlaThrThrLysGlu......
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...AlaGluGlyLysLeuArgGluLeuHis.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                ......ArgGlyGluTrp...AspGluLeu.....
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seq_documentation_block:
ID x20248 standard; DN
seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63094 GAGTTGGTCAATTTGAGGAAGGAAAGTTATCATTTTAAATCCCGATTTT 63045
                                                                                                                                                                                                                03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                       Claim 1; Page 157-671; 1128pp; English
                                                                                                                                   Clayton R, White OR;
                                                                                                                                                                                                                                                                                                                                                                                         Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235
                                                  and therapy of infections, particularly Lyme disease
                                                              New isolated Borrelia burgdorferi nucleic acids - used to products for the detection, diagnosis, characterisation, p
                                                                                                        WPI; 1999-081217/07.
                                                                                                                                                                                                                                                                                                               30-DEC-1998.
                                                                                                                                                                                                                                                                                                                                        WO9858943-A1
                                                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia burgdorferi polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-1999
                                                                                                                                                                         (HÜMA-)
                                                                                                                                                                                                                                                                                    18-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X20248 standard; DNA; 910715 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGAGTATAAATAAATCCTTAAATCTTAAGAAA......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spLeuLeuThrThrLeuIleGluCysAlaTyrPheSerValGlyLys 251
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                                                                                                                                                                          MEDIMMUNE
                                                                                                                                                                                       HUMAN GENOME SCI
                                                                                                                                              Dougherty BA,
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                                                                                                                                                                                                                97US-0057483.
97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                                                                                                          INC.
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                                                                                                                                               Fraser C,
                                                                                                                                               Lathigra
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                                                                prevention
                                                                              develop
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X20248 to X20402 represent polynucleotide sequences isolated from

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alignment_scores:
Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   491304 ATGGAAAGCCCAAGGCTGAAATGTGG...CTTGGAGCACACAAGACATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      491254 TGATTGGGGCGGAATTAATTTTATTCCCAATCTTTTGGGTGATAAGATTG 491303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         491351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 910715 BP; 327171 A; 129646 C; 130753 G; 323091 T; 54 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lyme disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MetThrThrGluProLeuPhePhe.....LysProValPheLysGluAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gIleTrpGlyGlyThrAlaLeuAlaAsp.....PheGlyTyrThrIleP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGAATAATGAAGATAATATTTTTTAATGAAAAATAATATTAAAGAATA 491253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rgPheProLeuLeuThrLysIleLeuAspAlaAspGlnAspLeuSerVal 94
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GATCTTATTGATAATTTTAGGGGCTATTGGTTTAATGAAATTTACAATAT
                                                                                                                                                                                                                               AAATTTCGACTTTCAATCACATAAAGATTTTGTAAAGACTATTTTGATT 491735
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCCCAAAATTGAACTTATTATGCTCTTAGTGATTTTTATGCTCTTAAA 491635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAATTCATCCTTCTAAAGATATTGCCTTAAAAGGGTATGAATCAGAGAA 491535
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                                                                                                               TACAAATGTATGAACTTGAGAAGATTATTGAAAAAATTTTAAAAAATTTG
                                                                                                                                                                                                                                                                                                                                           GGCTTTTTACCCTTAGATGAGATTAAAAAAATTTATGAAATTCTGGAATT 491685
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                                                                                                                                                                                                                                                                                                                                                                                                  .....AspCysGlnLysAspAlaGluIleIle....
                                                .....ArgGlyGluTrp...AspGluLeu.....
                                                                                                                                                                                                                                                                                  .....TyrGlyHisAsnAlaThrThrLysGlu......
                                                                                                                                                                     .GluLeuThrThrMetIleGlu......
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46.305
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Identity:
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22
23.645
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   491835
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seq_documentation_block:
ID A54211 standard; DNA;
XX
AC A54211;
XX
DT 26-FEB-2001 (first e
XX
Transformation vector
XX
Tricothecene resistar
KW fungus; wheat; maize;
KW transformation; Fusar
XX
Synthetic.
XX
PD W0200060061-A2.
XX
PD 12-OCT-2000.
XX
PD 12-OCT-2000.
XX
29-MAR-2000; 2000WO-1
XX
31-MAR-1999; 99US-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492033 GAGTTGGTCAATTTGAGGAAAGAAGTTATCATTTTTAAATCCCGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           492133 TCAAAAAAAAAATAAATGAGAACATTTGTATTAATAGAAATAGTGCAATGG 492182
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                                                                                                                                                                                                                                                Tricothecene resistance; resistant; fungus; wheat; maize; barley; rice; transformation; Fusarium; ds.
                                                                                                                                                                                                                                                                                                                                                   Transformation vector pCIB9818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A54211 standard; DNA; 6111 BP
                                                        29-MAR-2000; 2000WO-EP02769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTATAGGTAAAAAAGCAGAAAACTTGTTTATTGAT...GGGGACGGCGAA 492298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TrpAsnLeuSerGlySerAlaSerLeuLysGlnGlnLysProPheLeuLe
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                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
            99US-0282995
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                                                                                                                                                                                                                                                                         crop protection;
heterologous gen
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alignment_scores:
    Quality:
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US-09-462-846-2 x A54211
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          2341
                                                                                                            2309
                                                                                                                                                                                                        2259 TGCCTTTCCTGTTCAAAGTATTATGCGCAGCACAGCCACTCTCCATTCAG
                                                           112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2112 CGATGGCCGAGCTGTGG...ATGGGCGCACATCCGAAAAGCAGTTCACGA 2158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2012 CCGATCATGCAAAAACTCATTAACTCAGTGCAAAACTATGCCTGGGGCAG 2061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A heterologous gene encoding a gene product which confers trichothecene resistance can be used to transform plant cells to make them resistant to fungal infection. The transformation method is useful for preventing mycotoxin contamination of a plant, particularly a crop plant such as wheat, maize, barley or rice, and for reducing and/or preventing the growth of a fungus of the genus fusarium that produces a trichothecene, preferably comprising a C-3 hydroxyl group, by growing transformed crop plants in an area which is moderate to severe fungal infestation. Plasmid pcIB9818 comprises the Zea mays ubiquitin promoter, the phosphate mannose lasmorase selectable marker and the cauliflower mosaic virus
                                                                                                                                  96 ValHisProAsnAspGluTyrAlaAsnIleHisGluAsnGlyGluLeugl 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6111 BP; 1503 A; 1457 C; 1439 G; 1712 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant cell for preventing mycotoxin contamination of wheat, maize, barley or rice plant, comprises heterologous polynucleotide encoding gene product expressed in cell, having trichothecene resistance
                                                                                                                                                                                                                                                                 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 52-54; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity
                                                                                                                                                                                                                                                                                                                                             66 sHisArgHis...LeuPheGlyGlnLeuGluGlyAspArgPhe...... 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 ValGlnAsnGlyMetTyrLysGlyPheThrLeuSerGluLeuTrpGluHi 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-679374/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NOVS ) NOVARTIS AG. (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 rgThrGlyGluCysTrpAlaPheAlaAlaHisGlnAsnGlyGlnSerVal 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 ProValPheLysGluArgIle......TrpGlyGl 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hohn TM, Peters C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-FEB-2000; 2000US-0502852.
                                                   Y . . . . . . . . . . . . . . . .
                                                                                                                                                                                                                                      ..ProLeuLeuThrLysIleLeuAspAlaAspGlnAspLeuSerValGln
TTTTGCCAAAGAAAATGCCGCAGGTATCCCGATGGATGCCGCCGAGCGTA 2390
                                                                                                    GTTCATCCAAAC......AAACACAATTCTGAAATCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145.50
0.841
43.467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Gaps:
Percent Identity:
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6:
                                                   6111
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17
21.357
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                                                                                                      2340
                                                                                                                                                                                                        2308
                                                                                                                                                                                                                                                           95
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seq_docum ID D021 XX	seq_name	30	30	N N	29	28	2	,2	2	Ν	2	u	N	N	N		2		2	
documentation_block:	ame: /SIDS6/gcgdata/geneseq/geneseqn/NA2001	283 yrValTyrProPheLysLysGlyAsp.HisMetLeuLeuPro :::       ::: :::            087 AGCAGTTACAGCTTAAACCGGGTGAATCAGCGTTATTGCCG	266 eLeuLeuIleSerValIIleGluGlyGluGlyArgMetIleSerGlyGluT ::::::::::::::::::::::::::::::::::::	250 GlyLysTrpAsnLeuSerGlySerAlaSerLeuLysGlnGlnLys ::::       :::  987 TCGCTGCATGACCTTAGTGATAAAGAAACCACCATTAGCCAGCAG	42 leGluCysAlaTyr	225 9HisThrValHisHisGluGlnIleGluAspLeuLeuThrThrThrLeuI ::: ::::::           ::: :887 TGTGAAATTCGAAGCCAAACCGGCTAACCAGTTGTTGACCCAGCCGGTGA	209 HisLeuLysLysSerIleGluVallleGluValProSerIleProGluAr :::    :::::   :::::: 2837 CGTGCGGGTCTGACGCCTAAATACATTGATATTCCGGAACTGGTTGCCAA	192 rgLeuTyrAspTyrAspArgLysAspAlaGluGlyLysLeuArgGluLeu         2834	175 yLysGlyIleLeuAlaLeuGluThrGlnGlnAsnSerAspThrThrTyr::::   :::   ::::    :::::::::::::::	159 LysProGlyAspPhePheTyrValProSerGlyThrValHisAlaIleGl :::      ::: :::::::::::::::::::::::::	152691 CGGAAGACAGCGGT	145 .GluargGlyGluTrpAspGlu	137 LysGluGluLeuThrThrMetIle	121AspCysGlnLysAspAlaGluIleIleTyrGlyHisAsnAlaThrThr     :::::::::::::::::::::::::::::::::	2491 CCAGCCGGTCGCAGGTGCACATCCGGCGATTGCTCACTTTTTACAACAGC	120	2441 TTCCTTGCGATGAACGCGTTTCGTGAATTTTCCGAGATTGTCTCCCTACT	120	2391 ACTATAAAGATCCTAACCACAAGCCGGAGCTGGTTTTTGCGCTGACGCCT	113LysThrGlu
	qn/NA2001.DAT:D02175	MetLeuLeuPro 296           CGTTTATTGCCG 3128		LeuLysGlnGlnLysProPh :::   ::: ACCATTAGCCAGCAGAGTGC					. >				TTTAAAATCGGCCCTCGATAG	TyrGlyHisAsnAlaThrThr ;;; GCCAGCCTGTTGAATATGCAG	TTGCTCACTTTTTACAACAGC		TTCCGAGATTGTCTCCCTACT		CTGGTTTTTGCGCTGACGCCT	CVeTroTvrTleTle
			283 3086	266 3036	249 2986	242 2936	225 2886	208 2836	192 2833	175 2790	158 2740	151 2690	144 2640	136 2590	2540	120	2490	120	2440	130

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Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid pZU634 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tomato;
                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potyvirus;
                                                                                                                                                                                                                                                                                                                promoter
                                                                                                                                                                                                                                                                                                                                                terminator
                                                                                                                                                                                                                                                                                                                                                                               repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                       intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                               stem_loop
                                                                                                                        misc_feature
                                                                                                                                                misc_feature
                                                                                                                                                                       misc_feature
                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_unit
                                                        08-MAY-2000;
                                                                                        WO200068374-A1
                                        10-MAY-1999;
                                                                         16-NOV-2000
Heifetz PB,
               (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                   _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is; PVY; virus
coat protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potato virus Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agrobacterium sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria.
                                                         2000WO-EP04117
Patton DA,
                                                                                                                                                                      /product= "Bacterial spectinomycin-detoxifying enzyme, aminoglycoside-3'-adenyltransferase" 8157..10244
                                                                                                                                                                                                                                                                                                                                                                              /label= Actin2_intronL complement (3057..3847)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "Ubiquitin3 (Ubi3) promoter plus leader
intron"
                                                                                                                      /label= pUC19_ORI
11195..11450
                                                                                                                                                                                                                                                              /product= "Phosphomannose isomerase 6623..6897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                 6949..7080
                                                                                                                                                                                                                                       /label= NOS
/note= "Agrobacterium
                                                                                                                                                                                                                                                                                         5386.,6561
                                                                                                                                                                                                                                                                                                                1193..5364
                                                                                                                                                                                                                                                                                                                       /label= NOS
/note= "Agrobacterium
                                                                                                                                                                                                                                                                                                                                                3855..4124
                                                                                                                                                                                                                                                                                                                                                       /rpt_type= INVERTED
/note= "Corresponds to
                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_type= INVERTED
/note= "Corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                        1790..2574
                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= b
/note= "Potato virus Y (PVY)
                                                                                                       /label= Nopaline_right_border_fragment
                                                                                                                                                10245..11179
                                                                                                                                                        /label= pVS1_ORI
                                                                                                                                                                                                             /*tag= j
/label= Nopaline_left_border_fragment
                                                                                                                                                                                                                                                                                              'tag= g
'label= SMAS_promoter
                                                                                                                                                                                                                                                                                                                                                                                                        595..3036
                                                                                                                                                                /*tag=
                                                                                                                                                                                                        359..8147
                                                                                                                                                                                                                                                         *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potato virus Y (PVY) resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              resistant; virus tolerant; CP; plasmid pZU634; ds.
                                                                                                                                         3
Levin JZ,
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Que Q,
                                                                                                                                                                                                                                                                                                                          nopaline
                                                                                                                                                                                                                                        nopaline synthase
                                                                                                                                                                                                                                                                                                                                                         γVq
                                                                                                                                                                                                                                                                                                                                                                                                               PVY coat protein (CP) region
                                                                                                                                                                                                                                                                                                                                                         CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 inverted
De
                                                                                                                                                                                                                                                                                                                                                         region"
                                                                                                                                                                                                                                                                                                                         synthase terminator"
 Haan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in
 PT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat region"
                                                                                                                                                                                                                                         terminator"
  Gielen
  JJL;
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Altering the expression of a viral genome, to obtain cells, plananimals that are resistant or tolerant to viruses, comprises us sense and antisense RNA fragments that form double-stranded RNA molecule -
                                                                                                                                                   The present sequence is plasmid p2U634, a chimeric gene cassette comprising the coding sequence for coat protein (CP) from Potato Y (PVY). This plasmid comprises a ubiquitin3 (Ubi3) promoter plus
                                                                                                                                                                                                                                         preferably plant cells, animals or their progenies resistant or tolerant to viruses such as tospoviruses, potyviruses, potexviruses, tobamoviruses, luteoviruses, cucumoviruses, bromoviruses,
                                                                                                                                                                                                                                                                                                        second DNA sequence capable of expressing an antisense RNA fragment of the viral genome. The sense and antisense RNA fragments are capable of forming double-stranded RNA. The method is useful for rendering cells,
                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to methods of altering the expression a viral genome, comprising introducing into a cell, a first DNA seq capable of expressing a sense RNA fragment of the viral genome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 14; Page 67-71; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecule
                                                                   leader intron, SMAS promoter, nopaline synthase (NOS) terminator, actin2 intront, pVS1 ORI, pUC19 ORI and coding sequences for phosphomannose isomerase A and bacterial spectinomycin-detoxifying enzyme, aminoglycoside-3'-adenyltransferase. This plasmid is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-007392/01
                                                                                                                                                                                                                         closteoviruses, tombusviruses and furoviruses.
Sequence 11461 BP; 3128 A; 2581 C;
                                            confer resistance to PVY in tomato
       2645 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to obtain cells, plants
viruses, comprises using
       3107 T;
       0 other
                                                                                                                                                                                                                                                                                                                                                                                                        g the expression
a first DNA sequ
                                                                                                                                                              promoter plus
                                                                                                                                                                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                                        virus
                                                                             б
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alignment\_block: US-09-462-846-2 x D02175 alignment\_scores: Align seg 1/1 to: D02175 Percent Similarity: 5430 5527 5480 CGATGGCCGAGCTGTGG...ATGGGCGCACATCCGAAAAAGCAGTTCACGA 5380 CCGATCATGCAAAAACTCATTAACTCAGTGCAAAACTATGCCTGGGGCAG 5677 5627 5577 112 19 y...ThrAlaLeuAlaAsp...PheGlyTyrThrIlePro...SerGlnA 33 66 50  $\mathfrak{S}$ 96 10 ProValPheLysGluArgIle......TrpGlyGl ValHisProAsnAspGluTyrAlaAsnIleHisGluAsnGlyGluLeuGl GTGCAGAATGCCGCCGGAGATATCGTTTCACTGCGTGATGTGATTGAGAG ValGlnAsnGlyMetTyrLysGlyPheThrLeuSerGluLeuTrpGluHi  ${\tt rgThrGlyGluCysTrpAlaPheAlaAlaHisGlnAsnGlyGlnSerVal}$ GTTCATCCAAAC TGCCTTTCCTGTTCAAAGTATTATGCGCAGCACAGCCACTCTCCATTCAG .ProLeuLeuThrLysIleLeuAspAlaAspGlnAspLeuSerValGln TGATAAATCGACTCTGCTCGGAGAGGCCGTTGCCAAACGCTTTGGCGAAC SHisArgHis...LeuPheGlyGlnLeuGluGlyAspArgPhe..... y..... Quality: Ratio: 145.50 0.841 43.467 from: Percent Identity: .... AAACACAATTCTGAAATCGG to: Length: Gaps: 398 17 21.357 5626 5576 5479 5429 19 66 49 5708 112 5676 79 112 95

5709

TTTTGCCAAAGAAATGCCGCAGGTATCCCGATGGATGCCGCCGAGCGTA 5758

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                                                                                                                                                                                                                                          6455 AGCAGTTACAGCTTAAACCGGGTGAATCAGCGTTTATTGCCG 6496
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                                                                                                                                                                                                                                                                                     yrValTyrProPheLysLysGlyAsp.HisMetLeuLeuPro 296
                                                                                                                                                                                                                                                                                                                                                                                    eLeuLeuIleSerValIleGluGlyGluGlyArgMetIleSerGlyGluT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGCTGCATGACCTTAGTGATAAAGAAACCACCATTAGCCAGCAGAGTGC 6404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACAAGGTGCAGAACTGGACTTCCCGATTCCAGTGGATGATTTTGCCTTC 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leGluCysAlaTyr.....PheSerVal 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HisLeuLysLysSerIleGluValIleGluValProSerIleProGluAr 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysProGlyAspPhePheTyrValProSerGlyThrValHisAlaIleG1 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGAAGACAGCGGTCTGTTCTCCCCGCTATTGCTGAATGTGGTGAAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGCAGGGTGAACCGTGGCAAACGATTCGTTTAATTTCTGAATTTTACC 6058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysGluGluLeuThrThrMetIle.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGATGCCGAACGTTTAAGCGAACTGTTCGCCAGCCTGTTGAATATGCAG 5958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGCCGGTCGCAGGTGCACATCCGGCGATTGCTCACTTTTTACAACAGC 5908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCCTTGCGATGAACGCGTTTCGTGAATTTTCCGAGATTGTCTCCCTACT 5858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTATAAAGATCCTAACCACAAGCCGGAGCTGGTTTTTGCGCTGACGCCT 5808
                                                                                                                                                                                                                                                                                                                                                    CGCCATTTTGTTCTGCGTCGAAGGCGATGCAACGTTGTGGAAAGGTTCTC 6454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyLysTrpAsnLeuSerGlySerAlaSerLeuLysGlnGlnLysProPh 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTGAAATTCGAAGCCAAACCGGCTAACCAGTTGTTGACCCAGCCGGTGA 6304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTGCGGGTCTGACGCCTAAATACATTGATATTCCGGAACTGGTTGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAAGGCGTG...GCGCTGGAAGTGATGGCAAACTCCGATAACGTG.... 6201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yLysGlyIleLeuAlaLeuGluThrGlnGlnAsnSerAspThrThrTyrA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACCCTGGCGAAGCGATGTTCCTGTTCGCTGAAACACCGCACGCTTACCT 6158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTGAAGAAAAATCCCGCGCGCGCTGGCGATTTTAAAATCGGCCCTCGATAG 6008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..AspCysGlnLysAspAlaGluIleIleTyrGlyHisAsnAlaThrThr 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rgLeuTyrAspTyrAspArgLysAspAlaGluGlyLysLeuArgGluLeu 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .GluArgGlyGlu...TrpAspGlu......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....LeuLeuArgArgValLysVal 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .......TysThrGluCysTrpTyrIleIle.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....CTG
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Chimeric - Bacteria.
Chimeric - Agrobacterium sp
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric -
Chimeric -
                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Кеу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potyvirus; ZYMV; PRSV; virus resistant; virus tolerant; melon; coat protein; CP; plasmid pZU623; ds.
16-NOV-2000
                                                     misc_feature
                                                                               misc_feature
                                                                                                          misc_feature
                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                    promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stem_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid
                  WO200068374-A1
                                                                                                                                                                                                             terminator
                                                                                                                                                                                                                                                                                                      terminator
                                                                                                                                                                                                                                                                                                                                         repeat_unit
                                                                                                                                                                                                                                                                                                                                                                             repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                       intron
                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p2U623 for ZYMV and PRSV resistance in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zucchini yellow mosaic virus.
Papaya ringspot virus.
Bacteria.
                                                                                                         aminoglycoside-3'-adenyltransférase"
9462..11549
                                                                                                                                                                                                                                                                                                                                        /rpt_type= INVERTED /note= "Corresponds to complement (4503..5143)
                                                                                                                                                                                                                                                                                                                                                                                                                                 2511..3111
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 55..1781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    **tag= a
/note= "Ubiquitin3 (Ubi3) promoter plus leader
intron"
                                                                                                                                                                                                                                                                                                     /*tag= g
/note= "PRSV CP region"
/note= "Corresponds to PRSV CP region"
5160..5429
                                                                                                                                                                                                                                                                                                                                                                       /label= Actin2_intronL
complement (3822..4422)
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1790..5143
                                                                                                                                                                       /label= NOS
/note= "Agrobacterium nopaline synthase terminator"
254.8385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
/note= "PRSV-ZYMV inverted repeat fragment"
                                     label=
                                                   'label= pUC19_ORI
.2500..12755
                                                                                                                             product= "Bacterial spectinomycin-detoxifying enzyme
                                                                                                                                                  '*tag= 1
'label= Nopaline_left_border_fragment
                                                                                                                                                                                                             /product= "Phosphomannose isomerase
1928..8202
                                                                                                                                                                                                                                      *tag= i
/label= SMAS_promoter
691..7866
                                                                                                                                                                                                                                                                 *tag= h
|Tabel= NOS
|Toote= "Agrobacterium nopaline synthase terminator"
| 498..6669
                                                                                                                                                                                                                                                                                                                                                                                                       245..3686
                                                                                                                                                                                                                                                                                                                                                                                                                rpt_type= INVERTED
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'note= "Corresponds
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                                                                              *tag= n
label= pVS1_ORI
1550..12484
                                                                                                                                               664..9452
                                  Nopaline_right_border_fragment
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                                                                                                                                                                                                                                                                                                                                                  ZYMV
                                                                                                                                                                                                                                                                                                                                                                                                                 VMYZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRSV coat protein (CP) region"
                                                                                                                                                                                                                                                                                                                                                                                                                CP region
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                                                                                                                                                                                                                                                                                                                                                  region'
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alignment_block:
US-09-462-846-2 x D02174
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    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio: Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: D02174 from: 1 to: 12766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6735
                                                                                                                                                                                                             6832 GTGCAGAATGCCGCCGGAGATATCGTTTCACTGCGTGATGTGATTGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6685 CCGATCATGCAAAAACTCATTAACTCAGTGCAAAACTATGCCTGGGGCAG 6734
                                                                        6882 TGATAAATCGACTCTGCTCGGAGAGGCCGTTGCCAAACGCTTTGGCGAAC 6931
                                                                                                                                                                                                                                                                                                                                               6785 CGATGGCCGAGCTGTGG...ATGGGCGCACATCCGAAAAGCAGTTCACGA 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is plasmid pZU623, a chimeric gene cassette comprising the coding sequence for coat protein (CP) from Zucchini yellow mosale virus (ZYMY) and papaya ringspot virus (PRSY). This plasmid also comprises a ubiquitin3 (Ubi3) promoter plus leader intron. SMAS promoter, nopaline synthase (NOS) terminator, actin2 intronL, PWS1 ORI, pUC19 ORI and coding sequences for phosphomannose isomerase A and bacterial spectinomycin-detoxifying enzyme, aminoglycoside-3'-adenyltransferase. This plasmid is used to confer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to methods of altering the expression of a viral genome, comprising introducing into a cell, a first DNA sequence capable of expressing a sense RNA fragment of the viral genome and a second DNA sequence capable of expressing an antisense RNA fragment of the viral genome and an artisense RNA fragment of the viral genome. The sense and artisense RNA fragments are capable of forming double-stranded RNA. The method is useful for rendering cells, preferably plant cells, animals or their progenies resistant or tolerant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Altering the expression of a viral genome, to obtain cells, plants or animals that are resistant or tolerant to viruses, comprises using sense and antisense RNA fragments that form double-stranded RNA molecule -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tobamoviruses, luteoviruses, cucumoviruses, bromoviruses, closteoviruses, tombusviruses and furoviruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; Page 62-65; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heifetz PB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAY-2000; 2000WO-EP04117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12766 BP; 3472 A; 2890 C; 2955 G; 3449 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resistance to ZYMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to viruses such as tospoviruses, potyviruses, potexviruses,
                                                                                                                                                                                                                                                                           50 ValGlnAsnGlyMetTyrLysGlyPheThrLeuSerGluLeuTrpGluHi 66
                                                                                                                                                                                                                                                                                                                                                                                          33 rgThrGlyGluCysTrpAlaPheAlaAlaHisGlnAsnGlyGlnSerVal 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 y...ThrAlaLeuAlaAsp...PheGlyTyrThrIlePro...SerGlnA 33 : ||||||||||||
80 ..ProLeuLeuThrLysIleLeuAspAlaAspGlnAspLeuSerValGln 95
                                                                                                                                 66 sHisArgHis...LeuPheGlyGlnLeuGluGlyAspArgPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 ProvalPheLysGluArgIle......TrpGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patton DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0309038
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0.841
43.467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Levin JZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 398
Gaps: 17
Percent Identity: 21.357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Que Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      De Haan
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                                                                                                                                                                                                             6881
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	3 yrValTyrProPheLysLysGlyAsp.HisMetLeuLeuPro 296	28:
7759	O CGCCATTTTGTTCTGCGTCGAAGGCGATGCAACGTTGTGGAAAGGTTCTC	7710
283	6 eLeuLeuIleSerValIleGluGlyGluGlyArgMetIleSerGlyG	26
266 7709	O GlyLysTrpAsnLeuSerGlySerAlaSerLeuLysGlnGlnLysProPh ::: ::: :::       ::: ::: :::    ::: 0 TCGCTGCATGACCTTAGTGATAAAGAAACCACCATTAGCCAGCAGGTGC	250 7660
7659	:::	7610
249	leGluCysAlaTyr	242
242 7609	5 gHisThrValHisHisGluGlnIleGluAspLeuLeuThrThrThrLeuI ::: ::::::::::::::::::::::::::::::::	225 7560
	CGTGCGGGTCTGACGCCTAAATACATTGATATTCCGGAACT	7510
225	HisLeuLysLysSerIleGluValIleGluValProSerIleProGlu	209
7509	7	7507
208	${\tt rgLeuTyrAspTyrAspArgLysAspAlaGluGlyLysLeuArgGlugluglugluglugluglugluglugluglugluglugl$	192
7506	Type of the second control of the second con	7464
192	v.vsClv1lalellalellalellalellalellalelalelalela	170
7463	LYSETOULYASPENEMENTYTYALFOSETULYTITVALHISALALIEGI   Y LYSETOULYASPENEMENTYTYALFOSETULYTITVALHISALALIEGI   AACCCTGGCGAAGCGATGTTCCTGTTCGCTGAAACACCGCACGCTTACCT   AACCCTGGCGAAGCGATGTTCCTGTTCGCTGAAACACCGCACGCTTACCT	7414
1 1		1 0
158	2	15:
7363	${\tt CCAGCAGGGTGAACCGTTGGCAAACGATTCGTTTAATTTCTGL}$	7314
51	.GluArgGlyGluTrpAspGlu	145
7313	4 GGTGAAGAAAATCCCGCGCGCT	7264
144	LysGluGluLeuThi	137
7263	CTGATGCCGAACGTTTAAGCGAAC	7214
136	AspCysGlnLysAspAlaGluIleIleTyI	121
7213	4 CCAGCCGGTCGCAGGTGCACATCCGGCGATTGCTCACTTTTTACAACAGC	7164
120	0	120
7163	4 TTCCTTGCGATGAACGCGTTTCGTGAATTTTCCGAGATTGTCTCCCTACT	7114
120	0	120
7113	ACTATAAAGATCCTAACCACAAGCCGGAGCTGGTTTTTGCGCTGACGCCT	7064
120	LysThrGluCysTrpTyrIleIl	113
7063	TTTTGCCAAAGAAAATGCCGCAGGTATCCCGATGGATGCCGCCGAGCGTA	7014
112	Y	112
112 7013	ValHisProAsnAspGluTyrAlaAsnIleHisGluAsnGlyGluLeuGl	96 6982
6981	:::       :::	6932

7760 AGCAGTTACAGCTTAAACCGGGTGAATCAGCGTTTATTGCCG 7801

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alignment_block:
                                                                                                                                                                                                                         alignment_scores:
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ID A54213 standard; DNA; 12949 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT:A54213
                                                                                                                                                                                                                                               A heterologous gene encoding a gene product which confers
C trichothecene resistance can be used to transform plant cells to
C make them resistant to fungal infection. The transformation method is
Useful for preventing mycotoxin contamination of a plant,
C particularly a crop plant such as wheat, maize, barley or rice, and
C for reducing and/or preventing the growth of a fungus of the genus
C Fusarium that produces a trichothecene, preferably comprising a C-3
C hydroxyl group, by growing transformed crop plants in an area which
C comprises the Zea mays ubiquitin promoter, the phosphate mannose
C isomorase selectable marker and the nopaline synthase
C termination sequence. pNOV1704 further comprises the Zea mays
Usiquitin promoter operably linked to the trichothecene 3-0-acetyl
C transferase sequence given in GENESEQ record A54206 and the nos
C termination sequence.
                                               Align seg 1/1 to: A54213 from:
                                                                              US-09-462-846-2 x A54213
                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tricothecene resistance; resistant; fungus; wheat; maize; barley; rice; transformation; Fusarium; ds.
                                                                                                                                                                                                                      Sequence 12949 BP; 3194 A; 3146 C; 3143 G; 3466 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 58-62; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant cell for preventing mycotoxin contamination of wheat, maize, barley or rice plant, comprises heterologous polynucleotide encoding gene product expressed in cell, having trichothecene resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-1999; 99US-0282995.
11-FEB-2000; 2000US-0502852.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hohn TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAR-2000; 2000WO-EP02769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
   2000-679374/66.
                                                                                                                                           Quality:
Ratio:
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                                                                                                                            145.50
0.841
43.467
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Gaps:
Percent Identity:
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                                               12949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               crop protection;
heterologous gene
                                                                                                                          398
17
21.357
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.TrpGlyG1 19
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2885	::::::::::::::::::::::::::::::::::::::	2836
225	isLeuLysLysSerIleGluValIleGluValProSerIleProGluAr	209
2835	CTG	2833
208	rgLeuTyrAspTyrAspArgLysAspAlaGluGlyLysLeuArgGluLeu	192
80 (		9
٥	vsGlvIleLeuAlaLeuGluThrGlnGlnAsnSerAspThrThrTvrA	175
2789	  CGCACGCTTACCT	2740
175	.ysProGlyAspPhePheTyrValProSerGlyThrValHisAl	159
158 2739	LeuLeuArgArgValLysVal	152 2690
2689	GGGTGAACCGTGGCAAACGATTCGTTTAATTTTCTGAATTTTTACC	4
151	luArgGlyGluTrpA	145
2639	AAGAAAATCCCGCGCGCTGGCGATTTTAAAATCGGCCCTCGATAG	2590
144	luLeuThrThrMetIl	137
2589	CCGAACGTTTAAGCGAACTGTTCGCCAGCCTGTTGAATATGCAG	2540
136	spCysGlnLysAspAlaGluIleIleTyrGlyHisAsnAlaThrThr	121
2539	CCAGCCGGTCGCAGGTGCACATCCGGCGATTGCTCACTTTTTACAACAGC	2490
120		120
2489	TTCCTTGCGATGAACGCGTTTCGTGAATTTTCCGAGATTGTCTCCCTACT	2440
120		120
2439	ACTATAAAGATCCTAACCACAAGCCGGAGCTGGTTTTTGCGCTGACGCCT	2390
120	ysTrpTyrIleIle	113
2389	TTTGCCAAAGAAAATGCCGCAGGTATCCCGATGGATGCCGCCGAGCGTA	2340
112	Y	112
112 2339	ValHisProAsnAspGluTyrAlaAsnIleHisGluAsnGlyGluLeuGl            	96 2308
2307	CTTTCCTGTTCAAAGTATTATGCGCAGCACAGCCACTCTCCATTC	2258
95	LeuThrLysIleLeuAspAlaAspGlnA 	80
2257	GATAAATCGACTCTGCTCGGAGAGGCCGTTGCCAAACGCT	2208
79	lyGlnLeuGluGlyAspArqPh	66
2207	ValGlnAsnGlyMetTyrLysGlyPheThrLeuSerGluLeuTpGluHi	2158
713/	GMI GGCCGAGCIGIGGAIGGGCGCACAICCCGAAAAGCAGTICA	1117
	gThrGlyGluCysTrpAlaPheAlaAlaHisGlnAsnGlyGlnSerVa	_
33 2110	YThrAlaLeuAlaAspPheGlyTyrThrIleProSerGlnA:	19 2061
2060	ACTCATTAACT	

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seq_documentation_block:
ID Z20087 standard; DNA; 6103 BP.
XX
AC Z20087;
XX
DT 05-JAN-2000 (first entry)
XX
CNISCTICIDE; HyFLIB; Crystal pro
KW crylB; CrylA(b); maize; transgen
KW polibella coli.
XX
Chimeric - Zea mays.
OS Chimeric - Zea mays.
OS Chimeric - Escherichia coli.
XX
Chimeric - Zea mays.
OS Chimeric - Escherichia coli.
XX
Chimeric - Zea mays.
OS Chimeric - Escherichia coli.
XX
Chimeric - Escherichia coli.
XX
Chimeric - Zea mays.
OS Chimeric - Escherichia coli.
XX
Chimeric - Zea mays.
OS Chimeric - Escherichia coli.
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Chimeric - Zea mays.
OS Chimeric - Escherichia coli.
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Chimeric - Zea mays.
OS Chimeric - Zea mays.
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OS Chimeric - Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2986 TCGCTGCATGACCTTAGTGATAAAGAAACCACCATTAGCCAGCAGAGTGC 3035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insecticide; HyFLIB; crystal protein; delta-endotoxin; toxin; crylB; cryLA(b); maize; transgenic plant; European corn borer Ostrinia nubilalis; entomocide; crop protection; biological copCIB9818; ubiquitin; promoter; mannose phosphate isomerase; pmi gene; selectable marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 eLeuLeuIleSerValIleGluGlyGluGlyArgMetIleSerGlyGluT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yrValTyrProPheLysLysGlyAsp.HisMetLeuLeuPro 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyLysTrpAsnLeuSerGlySerAlaSerLeuLysGlnGlnLysProPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cauliflower mosaic virus
                                                                                                                                                                                                                                                                                                                                                              /note= "beta-lactamase 6087..6103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= u
/note= "35S terminator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "inverted PEPC intron 2249..3426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= b
/note= "PMI gene"
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"lacz' gene"
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-462-846-2 x Z20087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
   2425
                                                                                                                             2375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2143 GTTCACGAGTGCAGAATGCCGCCGGAGATATCGTTTCACTGCGTGATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2096 CAGCCAGCCGATGGCCGAGCTGTGG...ATGGGCGCACATCCGAAAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2046 TGGGGCAGCAAAACGGCGTTGACTGAACTTTATGGTATGGAAAATCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2193 ATTGAGAGTGATAAATCGACTCTGCTCGGAGAGGCCGTTGCCAAACGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the nucleotide sequence of pCIB9818 Ubi/PMI selectable marker plasmid including the mannose phosphate isomerase (PMI) gene under control of the maize ubiquitin promoter. The invention describes the design and construction of a chimeric insecticidal protein, termed hyFLIB (see Y31990), encoded by a synthetic maize-optimized gene (see Y31990), and composed of a crylB core N-terminal toxin portion and a crylA(b) C-terminal protoxin portion. When HyFLIB is expressed in transgenic maize, insecticidal activity is observed against European corn borer 
                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Ostrinia nubilalis). Recombinant microbial strains transformed with the hyFLIB gene can be used in endotmocidal formulations for the biological control of Lepidopteran pests.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 78-80; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric insecticidal protein comprising cryIB and cryIA(b) portions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-601323/51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 .SerGlnArgThrGlyGluCysTrpAlaPheAlaAlaHisGlnAsnGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 TrpGlyGly...ThrAlaLeuAlaAsp...PheGlyTyrThrIlePro..
TGACGCCTTTCCTTGCGATGAACGCGTTTCGTGAATTTTCCGAGATTGTC
                                                                                                                                                                                                                                                                                                             GluLeuGly.....
                                                                                                                                                                                                                                                                                                                                                                                 CCATTCAGGTTCATCCAAAC......AAACACAATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGCGAACTGCCTTTCCTGTTCAAAGTATTATGCGCAGCACAGCCACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TrpGluHisHisArgHis...LeuPheGlyGlnLeuGluGlyAspArgPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lnSerValValGlnAsnGlyMetTyrLysGlyPheThrLeuSerGluLeu
                                                             1e.....
                                                                                                                                                                                                                                                       erValGlnValHisProAsnAspGluTyrAlaAsnIleHisGluAsnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e......ProLeuLeuThrLysIleLeuAspAlaAspGlnAspLeuS
                                                                                                                          CGAGCGTAACTATAAAGATCCTAACCACAAGCCGGAGCTGGTTTTTGCGC
                                                                                                                                                                                       .....LysThrGluCysTrpTyrIleI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
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Gaps: 16
Percent Identity: 21.615
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75	TCCCTACTCCAGCCGGTCGCAGGTGCACATCCGGCGATTGCTCACTTTTT :	52
21	spCysGlnLysAspAlaGluI	134
25	CCGAACGTTTAAGCGAACTGTT	257
34	luGluLeuThrThrMetIl	44
75	GAAAAATCCCGCGCG	262
45	luArgGlyG	51
25	GGGTGAACCGTGGC	267
52	LeuLeuArgArgV	156
75	TGCTGAATGT	272
56	lLysValLysProGlyAspPhePheTyrValProSerGlyThrValH	172
25	ATTGAACCCTGGCGAAGCGATGTTCCTGTTCGCTGAAACACCGCA	277
73	uGluThrGlnGlnAsnSerAs	[89]
75	TACCTGCAAGGCGTGGCGCTGGAAGTGATGGCAAACTCCGAT	282
89	rThrTyrArgLeuTyrAspTyrAspArgLysAspAlaGluGlyLysLeuA 2	909
22		82
90	euHisLeuLysLysSerIleGluValIleGluV	222
26	GCGTGCGGGTCTGACGCCTAAATACATTGATATTCCGGAACTG	287
23	isHisGluGlnIleGluAspLeuLeuT	239
71	TGTGAAATTCGAAGCCAAACCGGCTAACCAGTTGTTG	292
39	CysAlaTyr	247
21	GCCGGTGAAACAAGGTGCAGAACTGGACTTCCCGATTCCAGTGGATGATT 2	297
47	SerValGlyLysTrpAsnLeuSerGlySerAlaSerLeuLysGlnGln	263
71	TIGCCTTCTCGCTGCATGACCTTAGTGATAAAGAAACCACCATTAGCCAG	302
64	euIleSerValIleGluGlyGluGlyArgMetIle	280
21	CAGAGTGCCGCCATTTTGTTCTGCGTCGAAGGCGATGCAACGTTGTGGAA	307
80	rGlyGluTyrValTyrProPheLysLysGlyAsp.HisMetLeuLeuPro	296
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